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	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
-29		
-28		
-27		
-26		
-25		
-24		
-23		
-22	16 (MET)	2.1
-21	16 (ASP)	2.1
-20	51 (MET)	2.
-19	23 (ARG)	14.
-18	18 (VAL)	21.
-17	44 (PRO)	6.1
-16	43 (ALA)	6.3
-15	48 (GLN)	4.5
-14	47 (LEU)	4.6
-13	49 (LEU)	3.3
-12	27 (GLY)	12.
-11	49 (LEU)	3.4
-10	58 (LEU)	1.
-9	47 (LEU)	6.2
-8	55 (LEU)	4.2
-7	56 (TRP)	3.2
-6	43 (LEU)	6.9
-5	47 (PRO)	6.3
-4	33 (GLY)	9.5
-3	28 (THR)	11.
-2	24 (THR)	16.
-1	34 (GLY)	11.

PRECURSOR OF:

- 1) HK101'CL: HUMAN KAPPA LI
- 2) HK137'CL: HUMAN KAPPA LI
- 3) VKI-Chr1'CL: HUMAN KAPPA
- 4) RuVHCAMP'CL: HUMAN KAPPA
- 5) VKI-ZI'CL: HUMAN KAPPA I
- 6) 3D6'CL: HUMAN KAPPA LIGH
- 7) V108'CL: HUMAN KAPPA LIG
- 8) Vb'CL: HUMAN KAPPA LIGHT
- 9) Vb''CL: HUMAN KAPPA LIGH
- 10) HK102'CL: HUMAN KAPPA LI
- 11) 2A12'CL: HUMAN KAPPA LIG
- 12) 1B1'CL: HUMAN KAPPA LIGH
- 13) 2C12'CL: HUMAN KAPPA LIG
- 14) 1B11'CL: HUMAN KAPPA LIG
- 15) Vd'CL: HUMAN KAPPA LIGH
- 16) Va''CL: HUMAN KAPPA LIGH
- 17) Ve'CL: HUMAN KAPPA LIGH
- 18) V13'CL: HUMAN KAPPA LIGH
- 19) GM 607'CL: HUMAN KAPPA I
- 20) A3'CL: HUMAN KAPPA LIGH
- 21) RPHI6410'CL: HUMAN KAPPA
- 22) A2'CL: HUMAN KAPPA LIGH
- 23) A23'CL: HUMAN KAPPA LIGH
- 24) NG9'CL: HUMAN KAPPA LIGH
- 25) HIC (R)'CL: HUMAN KAPPA
- 26) HAH 14.1'CL: HUMAN KAPPA
- 27) HAH 14.2'CL: HUMAN KAPPA
- 28) HAH 16.1'CL: HUMAN KAPPA
- 29) NOV'CL: HUMAN KAPPA LIGH
- 30) SE10'CL: HUMAN KAPPA LIGH
- 31) TB3'CL: HUMAN KAPPA LIGH
- 32) Humkv325'CL: HUMAN KAPPA
- 33) EV1-15'CL: HUMAN KAPPA
- 34) IARC/BL41'CL: HUMAN KAPPA
- 35) Humkv305'CL: HUMAN KAPPA
- 36) LS1'CL: HUMAN KAPPA LIGH
- 37) LS2'CL: HUMAN KAPPA LIGH
- 38) LS4'CL: HUMAN KAPPA LIGH
- 39) LS5'CL: HUMAN KAPPA LIGH
- 40) LS6'CL: HUMAN KAPPA LIGH
- 41) LS7'CL: HUMAN KAPPA LIGH
- 42) LS8'CL: HUMAN KAPPA LIGH
- 43) Vg'CL: HUMAN KAPPA LIGH
- 44) Vh'CL: HUMAN KAPPA LIGH
- 45) CLL'CL: HUMAN KAPPA LIGH
- 46) Humkv328'CL: HUMAN KAPPA
- 47) Humka31as'CL: HUMAN KAPPA
- 48) GF4/1.1'CL: HUMAN KAPPA
- 49) K- EV15'CL: HUMAN KAPPA
- 50) VKAPPA IV GERMLINE'CL:
- 51) PB17IV'CL: HUMAN KAPPA
- 52) FK-001'CL: HUMAN KAPPA
- 56) HK100'CL: HUMAN KAPPA L
- 62) K- EVJK11'CL: HUMAN KAP

REFERENCE: SIGNAL PEPTI

- 1) HK101'CL: BENTLEY, D.L.
- 2) HK137'CL: BENTLEY, D.L.
- 3) VKI-Chr1'CL: LOTSCHER, E. 69, 215-223.
- 4) RuVHCAMP'CL: RIECHMANN,
- 5) VKI-ZI'CL: STRAUBINGER,
- 6) 3D6'CL: FELGENHAUER, M.,
- 7) V108'CL: HUBER, C., THIEE
- 8) Vb'CL: PECH, M., JAENICHE (CHECKED BY AUT)
- 9) Vb''CL: PECH, M., JAENICHE (CHECKED BY AUT)
- 10) HK102'CL: BENTLEY, D.L. LINDENMAIER, W.,
- 11) 2A12'CL: LEVY, S., MENDEL
- 12) 1B1'CL: LEVY, S., MENDEL
- 13) 2C12'CL: LEVY, S., MENDEL
- 14) 1B11'CL: LEVY, S., MENDEL
- 15) Vd'CL: PECH, M., JAENICHE (CHECKED BY AUT)
- 16) Va''CL: PECH, M., JAENICHE (CHECKED BY AUT)
- 17) Ve'CL: PECH, M., JAENICHE (CHECKED BY AUT)
- 18) V13'CL: JAENICHEN, H.-R. BY AUTHOR 12/1'
- 19) GM 607'CL: KLOBECK, H.G.
- 20) A3'CL: STRAUBINGER, B., (1988) J.MOL.B.
- 21) RPHI6410'CL: KLOBECK, H. LEDER, P. (1986)
- 22) A2'CL: SCOTT, M.G., CRIME
- 23) A23'CL: STRAUBINGER, B., (1988) J.MOL.B.
- 24) NG9'CL: BENTLEY, D.L. (
- 25) HIC (R)'CL: KIPPS, T.J.,
- 26) HAH 14.1'CL: KIPPS, T.J.
- 27) HAH 14.2'CL: KIPPS, T.J.
- 28) HAH 16.1'CL: KIPPS, T.J.
- 29) NOV'CL: KIPPS, T.J., TOM
- 30) SE10'CL: DERSIMONIAN, H.
- 31) TB3'CL: DERSIMONIAN, H.
- 32) Humkv325'CL: KIPPS, T.J.
- 33) EV1-15'CL: NEWKIRK, M.M.
- 34) IARC/BL41'CL: KLOBECK,
- 35) Humkv305'CL: CHEN, P.P. PROC. NATL. ACAD
- 36) LS1'CL: SILBERSTEIN, L.
- 37) LS2'CL: SILBERSTEIN, L.

PRECURSOR OF:

- 1) HK101'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 2) HK137'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 3) VKI-Chr1'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 4) HvHCAMP'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 5) VKI-SI'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 6) 3D6'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 7) V108'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 8) Vb'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 9) Vb'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 10) HK102'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 11) 2A12'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 12) 1B1'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 13) 2C12'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 14) 1B11'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 15) Vd'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 16) Va'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 17) Ve'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 18) V13'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP I
- 19) GM 607'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP II
- 20) A3'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP II
- 21) RPM16410'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP II
- 22) A2'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP II
- 23) A23'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP II
- 24) NG9'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 25) HIC (R)'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 26) HAE 14.1'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 27) HAE 14.2'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 28) HAE 16.1'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 29) NOV'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 30) SE10'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 31) TH3'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 32) Humkv325'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 33) EV1-15'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 34) IARC/BL41'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 35) Humkv305'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 36) LS1'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 37) LS2'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 38) LS4'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 39) LS5'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 40) LS6'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 41) LS7'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 42) LS8'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 43) Vg'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 44) Vh'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 45) CLL'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 46) Humkv328'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 47) Humka31es'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 48) GF4/1.1'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 49) K-EV15'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP III
- 50) VKAPPA IV GERMELINE'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP IV
- 51) PB17IV'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP IV
- 52) FR-001'CL: HUMAN KAPPA LIGHT CHAINS SUBGROUP IV
- 56) HK100'CL: HUMAN KAPPA LIGHT CHAIN OF HK100
- 62) K-EVJK11'CL: HUMAN KAPPA PSEUDOGENE

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- 1) HK101'CL: BENTLEY, D.L. & RABBITTS, T.H. (1980) NATURE, 288, 730-733. (CHECKED BY AUTHOR 11/30/82)
- 2) HK137'CL: BENTLEY, D.L. & RABBITTS, T.H. (1983) CELL, 32, 181-189.
- 3) VKI-Chr1'CL: LOTSCHER, E., ZIMMER, F.-J., KLOPSTOCK, T., GRZESCHIK, K.-H., JAENICHEN, R., STRAUBINGER, B. & ZACHAU, H.G. (1988) GENE, 69, 215-223.
- 4) HvHCAMP'CL: RIECHMANN, L., CLARK, M., WALDMANN, H. & WINTER, G. (1988) NATURE, 332, 323-327.
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- 6) 3D6'CL: FELGENHAUER, M., KOHL, J. & RUKER, F. (1990) NUCL. ACIDS RES., 18, 4927.
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- 8) Vb'CL: PECH, M., JAENICHEN, H.-R., POHLNIZ, H.-D., NEUMAIER, P.S., KLOBECK, H.-G. & ZACHAU, H.G. (1984) J. MOL. BIOL., 176, 1-16. (CHECKED BY AUTHOR 12/14/84)
- 9) Vd'CL: PECH, M., JAENICHEN, H.-R., POHLNIZ, H.-D., NEUMAIER, P.S., KLOBECK, H.-G. & ZACHAU, H.G. (1984) J. MOL. BIOL., 176, 1-16. (CHECKED BY AUTHOR 12/14/84)
- 10) HK102'CL: BENTLEY, D.L. & RABBITTS, T.H. (1980) NATURE, 288, 730-733. (CHECKED BY AUTHOR 11/30/82); JAENICHEN, H.-R., PECH, M., LINDENMAIER, W., WILDGRUBER, N. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 5249-5263.
- 11) 2A12'CL: LEVY, S., MENDEL, E., KON, S., AVNUR, Z. & LEVY, R. (1988) J. EXP. MED., 168, 475-489.
- 12) 1B1'CL: LEVY, S., MENDEL, E., KON, S., AVNUR, Z. & LEVY, R. (1988) J. EXP. MED., 168, 475-489.
- 13) 2C12'CL: LEVY, S., MENDEL, E., KON, S., AVNUR, Z. & LEVY, R. (1988) J. EXP. MED., 168, 475-489.
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- 16) Va'CL: PECH, M., JAENICHEN, H.-R., POHLNIZ, H.-D., NEUMAIER, P.S., KLOBECK, H.-G. & ZACHAU, H.G. (1984) J. MOL. BIOL., 176, 1-16. (CHECKED BY AUTHOR 12/14/84)
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- 18) V13'CL: JAENICHEN, H.-R., PECH, M., LINDENMAIER, W., WILDGRUBER, N. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 5249-5263. (CHECKED BY AUTHOR 12/14/84)
- 19) GM 607'CL: KLOBECK, H.G., SOLOMON, A. & ZACHAU, H.G. (1984) NATURE, 309, 73-76. (CHECKED BY AUTHOR 06/27/85)
- 20) A3'CL: STRAUBINGER, B., HUBER, E., LORENZ, W., OSTERHOLZER, E., PARGENT, W., PECH, M., POHLNIZ, H.-D., ZIMMER, F.-J. & ZACHAU, H.G. (1988) J. MOL. BIOL., 199, 23-34.
- 21) RPM16410'CL: KLOBECK, H.G., MEINDL, A., COMBIATO, G., SOLOMON, A. & ZACHAU, H.G. (1985) NUCL. ACIDS RES., 13, 6499-6513; WEIR, L. & LEDER, P. (1986) NUCL. ACIDS RES., 14, 3957-3970.
- 22) A2'CL: SCOTT, M.G., CRIMMINS, D.L., MCCOURT, D.W., ZOCHER, I., THIEBE, R., ZACHAU, H.G. & NAHM, M.H. (1989) J. IMMUNOL., 143, 4110-4116. (1988) J. MOL. BIOL., 199, 23-34.
- 23) A23'CL: STRAUBINGER, B., HUBER, E., LORENZ, W., OSTERHOLZER, E., PARGENT, W., PECH, M., POHLNIZ, H.-D., ZIMMER, F.-J. & ZACHAU, H.G. (1988) J. MOL. BIOL., 199, 23-34.
- 24) NG9'CL: BENTLEY, D.L. (1984) NATURE, 307, 77-80.
- 25) HIC (R)'CL: KIPPS, T.J., TOMHAVE, E., CHEN, P.P. & CARSON, D.A. (1988) J. EXP. MED., 167, 840-852.
- 26) HAE 14.1'CL: KIPPS, T.J., TOMHAVE, E., CHEN, P.P. & CARSON, D.A. (1988) J. EXP. MED., 167, 840-852.
- 27) HAE 14.2'CL: KIPPS, T.J., TOMHAVE, E., CHEN, P.P. & CARSON, D.A. (1988) J. EXP. MED., 167, 840-852.
- 28) HAE 16.1'CL: KIPPS, T.J., TOMHAVE, E., CHEN, P.P. & CARSON, D.A. (1988) J. EXP. MED., 167, 840-852.
- 29) NOV'CL: KIPPS, T.J., TOMHAVE, E., CHEN, P.P. & FOX, R.I. (1989) J. IMMUNOL., 142, 4261-4268.
- 30) SE10'CL: DERSIMONIAN, H., MCADAM, K.P.W.J., MACKWORTH-YOUNG, C. & STOLLAR, B.D. (1989) J. IMMUNOL., 142, 4027-4033.
- 31) TH3'CL: DERSIMONIAN, H., MCADAM, K.P.W.J., MACKWORTH-YOUNG, C. & STOLLAR, B.D. (1989) J. IMMUNOL., 142, 4027-4033.
- 32) Humkv325'CL: KIPPS, T.J., TOMHAVE, E., CHEN, P.P. & CARSON, D.A. (1988) J. EXP. MED., 167, 840-852.
- 33) EV1-15'CL: NEWKIRK, M.M., GRAM, K., HEINRICH, G.F., OSTBERG, L., CAPRA, J.D. & WASSERMAN, R.L. (1988) J. CLIN. INVEST., 81, 1511-1518.
- 34) IARC/BL41'CL: KLOBECK, H.G., MEINDL, A., COMBIATO, G., SOLOMON, A. & ZACHAU, H.G. (1985) NUCL. ACIDS RES., 13, 6499-6513.
- 35) Humkv305'CL: CHEN, P.P., ALBRANDT, K., ORIDA, N.K., RADOUX, V., CHEN, E.Y., SCHRANTZ, R., LIU, F.-T. & CARSON, D.A. (1986) PROC. NATL. ACAD. SCI. USA, 83, 8318-8322. (CHECKED BY AUTHOR 10/06/87)
- 36) LS1'CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 37) LS2'CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.

REFERENCE: SIGNAL PEPTIDES OF HUMAN KAPPA LIGHT CHAINS (cont'd)

- 38) LS4'CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 39) LS5'CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 40) LS6'CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 41) LS7'CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 42) LS8'CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 43) Vg'CL: PECH, M. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 24, 9229-9236.
- 44) Vh'CL: PECH, M. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 24, 9229-9236.
- 45) CLL'CL: JIRIK, F.R., SORGE, J., FONG, S., HEITZMANN, J.G., CURD, J.G., CHEN, P.P., GOLDFIEN, R. & CARSON, D.A. (1986) PROC. NAT. ACAD. SCI. USA, 83, 2195-2199.
- 46) Humkv328'CL: CHEN, P.P., ROBBINS, D.L., JIRIK, F.R., KIPPS, T.J. & CARSON, D.A. (1987) J. EXP. MED., 166, 1900-1905.
- 47) Humka31es'CL: CHEN, P.P., ROBBINS, D.L., JIRIK, F.R., KIPPS, T.J. & CARSON, D.A. (1987) J. EXP. MED., 166, 1900-1905.
- 48) G4/1.1'CL: GILLIES, S.D., DORAI, H., WESOLOWSKI, J., MAJEAU, G., YOUNG, D., BOYD, J., GARDNER, J. & JAMES, K. (1989) BIO/TECH., 7, 799-804.
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- 50) VKAPPA IV GERMLINE'CL: KLOBECK, H.G., BORNKAMM, G.W., COMBRIATO, G., MOCIKAT, R., POHLENZ, H.D. & ZACHAU, H.G. (1985) NUC. ACIDS RES., 13, 6515-6529.
- 51) PB17IV'CL: MARSH, P., MILLS, F. & GOULD, H. (1985) NUC. ACIDS RES., 13, 6531-6544. (CHECKED BY AUTHOR 03/19/86).
- 52) FK-001'CL: NAKATANI, T., NOMURA, N., HORIGOME, K., OHTSUKA, H. & NOGUCHI, H. (1989) BIO/TECH., 7, 805-810.
- 53) WALKER'CL: KLOBECK, H.G., COMBRIATO, G. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 18, 6995-7006.
- 54) DAUDI'CL: KLOBECK, H.G., COMBRIATO, G. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 18, 6995-7006.
- 55) VJ1'CL: KLOBECK, H.G., BORNKAMM, G.W., COMBRIATO, G., MOCIKAT, R., POHLENZ, H.D. & ZACHAU, H.G. (1985) NUC. ACIDS RES., 13, 6515-6529.
- 56) HK100'CL: BENTLEY, D.L. & RABBITTS, T.H. (1980) NATURE, 288, 730-733. (CHECKED BY AUTHOR 11/30/82)
- 57) Va'CL: PECH, M., JAENICHEN, H.-R., POHLENZ, H.-D., NEUMAIER, P.S., KLOBECK, H.-G. & ZACHAU, H.G. (1984) J. MOL. BIOL., 176, 1-16. (CHECKED BY AUTHOR 12/14/84)
- 58) V2'CL: JAENICHEN, H.-R., PECH, M., LINDENMAIER, W., WILDGRUBER, N. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 5249-5263. (CHECKED BY AUTHOR 12/14/84)
- 59) V14'CL: JAENICHEN, H.-R., PECH, M., LINDENMAIER, W., WILDGRUBER, N. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 5249-5263. (CHECKED BY AUTHOR 12/14/84)
- 60) V52'CL: JAENICHEN, H.-R., PECH, M., LINDENMAIER, W., WILDGRUBER, N. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 5249-5263. (CHECKED BY AUTHOR 12/14/84)
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GENERAL NOTES: SIGNAL PEPTIDES OF HUMAN KAPPA LIGHT CHAINS

THE NUCLEOTIDE SEQUENCES OF DIFFERENT CLONES CONTAIN AN INTERVENING SEQUENCE OF NONTRANSLATED BASES OF VARYING LENGTHS. THE SPLICING OUT OF THESE INTRONS COULD OCCUR BETWEEN AMINO ACID POSITIONS -5 AND -4, OR -4 AND -3, OR WITHIN POSITION -4. HOWEVER, IF THE SPLICING REQUIRES GT AT THE 5'-END AND AG AT THE 3'-END OF THE INTRON, THIS WOULD DEFINE THE JOINING AS OCCURRING WITHIN THE CODON OF AMINO ACID RESIDUE -4. THE INTRON SIZES OF DIFFERENT SEQUENCES ARE LISTED BELOW:

CLONE:	SOURCE:	INTRON SIZE:
HK100'CL	HUMAN FETAL LIVER DNA	118
HK101'CL	HUMAN FETAL LIVER DNA	125
HK102'CL	HUMAN FETAL LIVER DNA	125
MOPC173B'CL	MOUSE ADULT DNA	121
S107B'CL	MOUSE ADULT MYELOMA DNA	175
L8'CL	MOUSE ADULT LIVER DNA	175
K2'CL	MOUSE EMBRYO DNA	118
MPC11'CL	MOUSE ADULT DNA	242
VKAPPA167'CL	MOUSE ADULT LIVER DNA	365
L6'CL	MOUSE ADULT LIVER DNA	113
L7'CL	MOUSE ADULT LIVER DNA	206
T1'CL	MOUSE ADULT MYELOMA DNA	113
T2'CL	MOUSE ADULT MYELOMA DNA	215
VT1/B'CL	MOUSE ADULT MYELOMA DNA	113
VTNP'CL	MOUSE HYBRIDOMA DNA	177

SPECIFIC NOTES: SIGNAL PEPTIDES OF HUMAN KAPPA LIGHT CHAINS

- 21) RPMI6410'CL: WEIR, L. & LEDER, P. FOUND POSITION -9 AS ARG INSTEAD OF MET.
- 25) HIC (R)'CL: FROM PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA.
- 26) HAH 14.1'CL: cDNA CLONE DERIVED FROM HAH(R).
- 27) HAH 14.2'CL: cDNA CLONE DERIVED FROM HAH(R).
- 28) HAH 16.1'CL: cDNA CLONE DERIVED FROM HAH(R).
- 29) NOV'CL: FROM EPSTEIN-BARR VIRUS TRANSFORMED SALIVARY GLAND LYMPHOCYTES OF PATIENT WITH PRIMARY SJOGREN'S SYNDROME 17.109-CRI+.
- 30) 8E10'CL: THIS HYBRIDOMA WAS GENERATED BY FUSION OF PERIPHERAL BLOOD CELLS OF A PATIENT WITH LEPROSY AND THE HUMAN MYELOBLASTOID CELL LINE GM4672.
- 31) TH3'CL: THIS HYBRIDOMA WAS GENERATED BY FUSION OF PERIPHERAL BLOOD CELLS OF A PATIENT WITH LEPROSY AND THE HUMAN MYELOBLASTOID CELL LINE GM4672.
- 45) CLL'CL: FROM HUMAN CHRONIC LEUKEMIA CELL WITH AN IgM ANTI-IgG
- 46) Humkv328'CL: GENE FOR HUMAN RHEUMATOID FACTORS.
- 47) Humka31es'CL: GENE FOR HUMAN RHEUMATOID FACTORS.
- 52) FK-001'CL: IT CAN BE EXPRESSED FUNCTIONALLY IN MOUSE MYELOMA CELLS.

SIGNAL PEPTIDES OF HUMAN LN

INVARIANT RESIDUES	1 189/F2 'CL	2 BL2 'CL	3 4G1 'CL
-21			
-20	MET	MET	MET
-19		ALA	THR
-18		GLY	CYS
-17		PHE	SER
-16		PRO	PRO
-15	LEU	LEU	LEU
-14		LEU	LEU
-13		LEU	LEU
-12		THR	THR
-11			
-10		LEU	LEU
-9		LEU	LEU
-8		THR	ILE
-7		HIS	HIS
-6	CYS(.95)	CYS	CYS
-5		ALA	THR
-4		GLY	GLY
-3		SER	SER
-2		TRP	TRP
-1		ALA	ALA

OCCURRENCES OF MOST COMMON AMINO ACID

	VARI
-21	
-20	15 (MET)
-19	8 (THR)
-18	11 (TRP)
-17	10 (THR)
-16	17 (PRO)
-15	18 (LEU)
-14	14 (LEU)
-13	12 (LEU)
-12	9 (THR)
-11	6 (THR)
-10	17 (LEU)
-9	17 (LEU)
-8	7 (LEU)
-7	15 (HIS)
-6	18 (CYS)
-5	15 (THR)
-4	17 (GLY)
-3	16 (SER)
-2	7 (+)
-1	9 (SER)

SIGNAL PEPTIDES OF HUMAN LAMBDA LIGHT CHAINS

INVIANT RESIDUES	1 189/F2 'CL '	2 BL2 'CL '	3 4G12 'CL '	4 T2 'CL '	5 T2 'CL '	6 Pog-B 'CL '	7 T1 'CL '	8 K6H6 'CL '	9 K4B8 'CL '	10 K5B8 'CL '	11 K5G5 'CL '	12 K5C7 'CL '	13 K6F5 'CL '	14 4A 'CL '	15 1B8 'CL '	16 Pag-1 'CL '	17 6H- 3C4 'CL '	18 H6- 3C4 'CL '	19 LHV 'CL '	# OF SEQUENCES	# OF AMINO ACIDS
-21	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	15	1
-20	ALA	THR	THR	THR	THR	ALA	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	15	2
-19	GLY	CYS	CYS	CYS	CYS	CYS	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	17	3
-18	PHE	SER	SER	SER	SER	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	17	4
-17	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	18	2
-16	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	18	1
-15	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	18	4
-14	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	18	3
-13	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	19	5
-12	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	19	2
-11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	19	3
-10	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	19	5
-9	THR	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	19	3
-8	THR	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	19	3
-7	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	19	2
-6	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	19	5
-5	ALA	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	19	4
-4	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	19	5
-3	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	19	4
-2	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	19	5
-1	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	19	4

OCCURRENCES
OF MOST COMMON
AMINO ACID

VARIABILITY

-21	15 (MET)	1.
-20	8 (THR)	3.7
-19	11 (TRP)	4.6
-18	10 (THR)	6.8
-17	17 (PRO)	2.1
-16	18 (LEU)	1.
-15	14 (LEU)	5.1
-14	12 (LEU)	4.5
-13	9 (THR)	11.
-12	6 (THR)	2.3
-11	17 (LEU)	2.2
-10	17 (LEU)	3.4
-9	7 (LEU)	14.
-8	15 (HIS)	3.8
-7	18 (CYS)	2.1
-6	15 (THR)	6.3
-5	17 (GLY)	3.4
-4	16 (SER)	4.7
-3	7 (+)	14.
-2	9 (SER)	8.4
-1		

ASES OF VARYING LENGTHS.
OR WITHIN POSITION -4.
EFINE THE JOINING AS
ISTED BELOW:

SJOGREN'S SYNDROME

PROSY AND THE HUMAN

ROSY AND THE HUMAN

PRECURSOR OF:

- 1) 1B9/F2'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I
- 2) BL2 'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I
- 3) 4G12'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I
- 4) T2:C5'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I
- 5) T2:C14'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I
- 6) Fog-B'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I
- 7) T1'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I
- 8) K6H6'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP II
- 9) K4B8'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP II
- 10) K5B8'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP II
- 11) K5G5'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP II
- 12) K5C7'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP II
- 13) K6F5'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP II
- 14) 4A'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP II
- 15) 1B8'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP III
- 16) Pag-1'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP III
- 17) 6H-3C4'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP IV
- 18) H6-3C4'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP IV
- 19) LBV'CL: HUMAN LAMBDA LIGHT CHAINS SUBGROUP VI

REFERENCE: SIGNAL PEPTIDES OF HUMAN LAMBDA LIGHT CHAINS

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- 2) BL2 'CL: TSUJIMOTO, Y. & CROCE, C.M. (1984) NUCLEIC ACIDS RES., 12, 8407-8414.
- 3) 4G12'CL: KISHIMOTO, T., OKAJIMA, H., OKUMOTO, T. & TANIGUCHI, M. (1989) NUCLEIC ACIDS RES., 17, 4385.
- 4) T2:C5'CL: BERINSTEIN, N., LEVY, S. & LEVY, R. (1989) SCIENCE, 244, 337-339.
- 5) T2:C14'CL: BERINSTEIN, N., LEVY, S. & LEVY, R. (1989) SCIENCE, 244, 337-339.
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- 11) K5G5'CL: LEVY, S., MENDEL, E., KON, S., AVNUR, Z. & LEVY, R. (1988) J. EXP. MED., 168, 475-489.
- 12) K5C7'CL: LEVY, S., MENDEL, E., KON, S., AVNUR, Z. & LEVY, R. (1988) J. EXP. MED., 168, 475-489.
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- 18) H6-3C4'CL: YAMASAKI, N., KOMORI, S. & WATANABE, T. (1987) MOL. IMMUNOL., 24, 981-985. (CHECKED BY AUTHOR 12/12/87)
- 19) LBV'CL: ANDERSON, M.L.M., BROWN, L., MCKENZIE, E., KELLOW, J.E. & YOUNG, B.D. (1985) NUC. ACIDS RES., 13, 8, 2931-2941. (CHECKED BY AUTHOR 08/21/85)

GENERAL NOTES: SIGNAL PEPTIDES OF HUMAN LAMBDA LIGHT CHAINS

THE NUCLEOTIDE SEQUENCES OF DIFFERENT CLONES CONTAIN AN INTERVENING SEQUENCE OF NONTRANSLATED BASES OF VARYING LENGTHS. THE SPLICING OUT OF THESE INTRONS COULD OCCUR BETWEEN AMINO ACID POSITIONS -5 AND -4, OR -4 AND -3, OR WITHIN POSITION -4. HOWEVER, IF THE SPLICING REQUIRES GT AT THE 5'-END AND AG AT THE 3'-END OF THE INTRON, THIS WOULD DEFINE THE JOINING AS OCCURRING WITHIN THE CODON OF AMINO ACID RESIDUE -4. THE INTRON SIZES OF DIFFERENT SEQUENCES ARE LISTED BELOW:

CLONE:	SOURCE:	INTRON SIZE:
S43'CL	MOUSE MYELOMA CDNA	
IG303LAMBDA'CL	MOUSE H2020 MYELOMA DNA	93
IG99LAMBDA'CL	MOUSE EMBRYO DNA	93
WES-IG13'CL	MOUSE EMBRYO DNA	93
MOPC315-26'CL'	MOUSE MYELOMA DNA	93
243'CL	CHICKEN SPLEEN CELL CDNA	

SPECIFIC NOTES: SIGNAL PEPTIDES OF HUMAN LAMBDA LIGHT CHAINS

- 1) 1B9/F2'CL: FROM A PATIENT WITH B CELL ACUTE LYMPHOCTIC LEUKEMIA WITH CHARACTERISTIC t(8;14) CYTOGENETIC TRANSLOCATION AT DIAGNOSIS.
- 3) 4G12'CL: IT RECOGNIZES A TUMOR-ASSOCIATED AND DIFFERENTIATION ANTIGEN OF MW 195,000.
- 6) Fog-B'CL: THREE-DIMENSIONAL MODEL HAS BEEN CONSTRUCTED FOR THIS ANTIBODY.
- 14) 4A'CL: FROM HUMAN CHROMOSOME 22 (LAMBDA LIGHT CHAIN)
- 15) Pag-1'CL: THREE-DIMENSIONAL MODEL HAS BEEN CONSTRUCTED FOR THIS ANTIBODY.
- 17) 6H-3C4'CL: 6H-3C4 IS AN ESTABLISHED HUMAN-MOUSE HETEROHYBRIDOMA WHICH SECRETES A HUMAN IGM-LAMBDA ANTIBODY. THIS SEQUENCE IS OBTAINED BY LIGATING THE VH GENE WITH HUMAN IGGL REGION. THE NEW HUMAN IGGL-LAMBDA ANTIBODY FULLY RETAINS THE ORIGINAL SPECIFICITY.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
-2	(TRP, LEU)

SIGNAL PEPTIDES OF MOUSE

INVARIANT	1	2
RESIDUES	SI07A	17/
	'CL	'CL

-29		---
-28	HIS	---
-27		---
-26		---
-25		---
-24		---
-23		---
-22		---
-21		---
-20		---
-19		---
-18		---
-17		---
-16		MET
-15		TYR
-14		ILE
-13		CYS
-12		LEU
-11		LEU
-10		SER
-9		ILE
-8		SER
-7		TYR
-6		CYS
-5		ARG
-4		CYS
-3		LEU
-2		VAL
-1		HIS

21	22	23
B603=	L XIX	10-25
46/2D7	27'CL	'CL
	'CL	

-29	---	---	---
-28	---	---	---
-27	---	---	---
-26	---	---	---
-25	---	---	---
-24	---	---	---
-23	---	---	---
-22	---	---	---
-21	---	---	---
-20	---	---	---
-19	MET	MET	MET
-18	LYS	LYS	LYS
-17	LEU	LEU	LEU
-16	PRO	PRO	PRO
-15	VAL	VAL	VAL
-14	ARG	ARG	ARG
-13	PRO	PRO	PRO
-12	LEU	LEU	LEU
-11	VAL	VAL	VAL
-10	LEU	LEU	LEU
-9	MET	MET	MET
-8	PHE	PHE	PHE
-7	TRP	TRP	TRP
-6	ILE	ILE	ILE
-5	PRO	PRO	PRO
-4	ALA	ALA	ALA
-3	SER	SER	SER
-2	SER	SER	SER
-1	SER	SER	SER

41	42	43	44
6F8	4D4	K18.1	RP9
'CL	'CL	'CL	'CL

-29	---	---	---
-28	---	---	---
-27	---	---	---
-26	---	---	---
-25	---	---	---
-24	---	---	---
-23	---	---	---
-22	---	---	---
-21	---	---	---
-20	---	---	---
-19	MET	MET	MET
-18	LYS	LYS	LYS
-17	LEU	LEU	LEU
-16	PRO	PRO	PRO
-15	VAL	VAL	VAL
-14	ARG	ARG	ARG
-13	LEU	LEU	LEU
-12	LEU	LEU	LEU
-11	VAL	VAL	VAL
-10	LEU	LEU	LEU
-9	MET	MET	MET
-8	PHE	PHE	PHE
-7	TRP	TRP	TRP
-6	ILE	ILE	ILE
-5	PRO	PRO	PRO
-4	ALA	ALA	ALA
-3	SER	SER	SER
-2	SER	SER	SER
-1	SER	SER	SER

SIGNAL PEPTIDES OF MOUSE KAPPA LIGHT CHAINS

	INVARIANT RESIDUES	1 S107A 'CL	2 17/9 'CL	3 198. 'CL	4 130. 'CL	5 198. 'CL	6 198. 'CL	7 180. 'CL	8 180. 'CL	9 6A4 'CL	10 D23 'CL	11 CL 'CL	12 180. 'CL	13 180. 'CL	14 180. 'CL	15 F6-3 'CL	16 B13 'CL	17 MB1 'CL	18 MRL- DNA10 'CL	19 K5.1 'CL	20 BC- 1004 'CL
-29																					
-28	HIS																				
-27																					
-26																					
-25																					
-24																					
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-2																					
-1																					

21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
 B003- L XIX 10-25 5-14 9-40 12-40 3-13 1d35.7 vk-1A MOPC vk-1Cf vk-1B 4-4-20 3-24 MRL-4 17C1 14C3 F1A5 vk-1C v1
 46/207 27'CL 'CL

-29																					
-28																					
-27																					
-26																					
-25																					
-24																					
-23																					
-22																					
-21																					
-20																					
-19	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
-18	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
-17	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-16	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
-15	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-14	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
-13	PRO	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-12	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-11	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-10	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-9	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
-8	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
-7	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
-6	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
-5	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
-4	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
-3	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
-2	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
-1	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER

41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61
 6F8 404 K18.1 RE93 17G5 36.5 W 42.4B 42.7 BXM-14 PAVK PAVK PAVK VK-24B 24B'CL 24B'CL 25-39'CL 25-47'CL 24.2'CL 24.1'CL 24A'CL 24C'CL 167'CL 167'CL 24A'CL
 'CL

-29																					
-28																					
-27																					
-26																					
-25																					
-24																					
-23																					
-22																					
-21																					
-20																					
-19	MET	MET	MET			ASN				MET	ARG	ARG	ARG	ARG	ARG	ARG	LYS		ARG	ARG	ARG
-18	LYS	LYS	LYS			LEU				SER	PHE	PHE	PHE	PHE	PHE	PHE	THR		CYS	CYS	CYS
-17	LEU	LEU	LEU			PRO				PRO	SER	SER	SER	SER	SER	SER	LEU		SER	SER	SER
-16	VAL	VAL	VAL			ALA				ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLN		LEU	ALA	ALA
-15	VAL	VAL	VAL			HIS				GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLU	GLU
-14	ARG	ARG	ARG			LEU				PHE	LEU	LEU	LEU	LEU	LEU	LEU	PHE		PHE	PHE	PHE
-13	LEU	LEU	LEU			LEU				PHE	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU
-12	LEU	LEU	LEU			VAL				PHE	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	ARG	ARG
-11	VAL	VAL	VAL			LEU				LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		VAL	LEU	LEU
-10	LEU	LEU	LEU			LEU				LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU
-9	MET	MET	MET			LEU				VAL	VAL	VAL	VAL	VAL	VAL	VAL	ILE		MET	VAL	VAL
-8	PHE	PHE	PHE			PHE				LEU	LEU	LEU	LEU	LEU	LEU	LEU	PHE		PHE	PHE	PHE
-7	TRP	TRP	TRP			TRP				TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP	TRP	TRP
-6	ILE	ILE	ILE			ILE				ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE
-5	PRO	PRO	PRO			PRO				ARG	ARG	ARG	ARG	ARG	ARG	ARG	PRO		SER	SER	SER
-4	ALA	ALA	ALA			THR				GLU	GLU	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY
-3	SER	SER	SER			SER				THR	THR	THR	THR	THR	THR	THR	THR		SER	SER	SER
-2	SER	SER	SER			SER				ASN	ASN	THR	THR	THR	THR	THR	THR		SER	SER	SER
-1	SER	SER	SER			GLY				GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY

12,6647-6661. (CHECKED BY
 CK,C.A.K. (1989) BIO/TECH.,

71,508-516.
 THOR 12/12/87)
 ,8,2931-2941. (CHECKED BY

BASES OF VARYING LENGTHS.
 OR WITHIN POSITION -4.
 DEFINE THE JOINING AS
 LISTED BELOW:

CYTOGENETIC TRANSLOCATION

MBDA ANTIBODY. THIS
 GG1-LAMBDA ANTIBODY FULLY

SIGNAL PEPTIDES OF MOUSE KAPPA LIGHT CHAINS (cont'd)

	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84
	MPC11	MOPC	16-10	21G	21A	21C	21A	21C	68F	MOPC	12C	13	14	15	MRL-22	MRL-22	VABE8	18-2-3	SD3	GG11	37A4	T3C	
	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	Histone-7	CL	CL	CL	CL	CL	CL	CL	CL
-29	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-28	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-27	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-26	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-25	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-24	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-23	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-22	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-21	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-20	MET	MET	MET	GLU	GLU	MET	MET	MET	MET	MET	MET	MET	MET	MET	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
-19	GLU	GLU	ASP	SER	LYS	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
-18	THR	THR	THR	ASP	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-17	ASP	ASP	ASP	THR	THR	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
-16	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
-15	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
-14	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
-13	LEU	LEU	LEU	TRP	TRP	LEU	LEU	LEU	LEU	LEU	LEU	LEU	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
-12	TRP	TRP	TRP	VAL	VAL	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-11	VAL	VAL	VAL	LEU	LEU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-10	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
-9	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
-8	LEU	LEU	LEU	TRP	TRP	LEU	LEU	LEU	LEU	LEU	LEU	ARG	LEU	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
-7	TRP	TRP	TRP	VAL	VAL	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
-6	VAL	VAL	VAL	PRO	PRO	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-5	PRO	PRO	PRO	GLY	GLY	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
-4	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
-3	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
-2	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
-1	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
	L8 ⁺ CL	S107B	T2(1)	38CV3	38CV4	V-K10	AS-A-8	7F11	2H1	H12	5-27	18C10	38C13	38C	PC613	38F13V	R8C173B	T1 ⁺ CL	CL	CL	L7 ⁺ CL
	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL
-29	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-28	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-27	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
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-25	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-24	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-23	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-22	MET	MET	MET	---	---	---	---	---	---	---	---	---	---	---	---	---	---	MET	---	---	---
-21	ASP	ASP	ASP	---	---	---	---	---	---	---	---	---	---	---	---	---	---	ASP	---	---	MET
-20	LEU	LEU	LEU	---	---	MET	---	MET	MET	MET	---	MET	---	---	MET	---	MET	MET	MET	MET	SER
-19	GLN	GLN	GLN	---	---	ILE	---	MET	MET	MET	MET	---	GLU	---	ARG	---	ARG	ARG	SER	SER	VAL
-18	VAL	VAL	VAL	---	---	ALA	---	SER	SER	SER	SER	SER	SER	SER	PRO	---	ALA	THR	VAL	VAL	PRO
-17	GLN	GLN	GLN	---	---	SER	---	SER	SER	SER	SER	SER	SER	SER	PRO	---	ALA	ALA	THR	THR	GLN
-16	ILE	ILE	ILE	---	---	ALA	---	ALA	ALA	ALA	ALA	ALA	ILE	ILE	ILE	---	GLN	GLN	GLN	GLN	VAL
-15	ILE	ILE	ILE	---	---	GLN	---	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	---	GLN	GLN	GLN	GLN	GLN
-14	SER	SER	SER	---	---	PHE	---	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	---	VAL	PHE	VAL	VAL	LEU
-13	PHE	PHE	PHE	---	---	LEU	---	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	PHE	LEU	LEU	LEU	GLY
-12	LEU	LEU	LEU	---	---	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	PHE	GLY	ALA	ALA	LEU
-11	LEU	LEU	LEU	---	---	LEU	---	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	GLY	GLY	ALA	ALA	LEU
-10	ILE	ILE	ILE	---	---	LEU	---	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	LEU	LEU	LEU	LEU	LEU
-9	ILE	SER	SER	---	---	SER	---	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	LEU	LEU	LEU	LEU	LEU
-8	VAL	VAL	VAL	---	---	VAL	---	VAL	VAL	VAL	VAL	VAL	PHE	PHE	PHE	---	LEU	LEU	LEU	LEU	TRP
-7	THR	THR	THR	---	---	CYS	---	CYS	CYS	CYS	CYS	CYS	TRP	TRP	TRP	---	TRP	TRP	TRP	TRP	LEU
-6	VAL	VAL	VAL	---	---	PHE	---	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	---	PHE	PHE	LEU	LEU	THR
-5	ILE	ILE	ILE	---	---	GLN	---	GLN	GLN	GLN	GLN	GLN	HIS	HIS	HIS	---	PRO	PRO	THR	THR	VAL
-4	MET	MET	MET	---	---	VAL	---	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY	GLY
-3	SER	SER	SER	---	---	THR	---	THR	THR	ALA	THR	THR	ALA	ALA	ALA	---	ALA	ILE			
-2	ARG	ARG	ARG	---	---	ASN	---	ARG	ARG	ARG	ARG	ARG	ARG	GLN	GLN	---	GLN	ARG	LYS	ARG	ARG
-1	GLY	GLY	GLY	---	---	CYS	---	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	---	CYS	CYS	CYS	CYS	CYS

	106 V33 'CL	107 10.2-8 'CL	108 V33 'CL	109 16 'CL	110 2-264 'CL	111 2-2C8 'CL	112 B16.2K1 'CL	113 UN34 'CL	114 C.AKR 'CL	115 SF/CamEi 'CL	116 PERA/EI 'CL	117 4.2. 6012 'CL	118 SK/CamRk 'CL	119 CB.5V 'CL	120 UN42 .5 'CL	121 BXN-16 'CL	122 UN42 'CL	123 C.C58 M75 'CL
-29	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-28	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-27	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-26	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-25	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-24	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-23	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-22	---	---	---	---	MET	---	---	MET	---	---	---	---	---	---	---	MET	MET	---
-21	---	---	---	---	ASP	---	---	ASP	---	---	---	---	---	---	---	ASP	ASP	---
-20	MET	---	MET	MET	MET	---	---	MET	MET	MET	MET	MET	MET	---	MET	MET	ILE	MET
-19	LYS	---	ARG	ARG	ARG	---	---	ARG	LYS	LYS	LYS	GLU	LYS	---	---	ARG	ARG	---
-18	PHE	---	THR	THR	ALA	---	---	ALA	SER	SER	SER	SER	SER	---	---	ALA	ALA	---
-17	PRO	---	PRO	PRO	GLN	---	---	GLN	GLN	GLN	GLN	GLN	GLN	---	---	PRO	PRO	---
-16	SER	---	ALA	ALA	ALA	---	---	ALA	THR	THR	THR	THR	THR	---	---	ALA	ALA	---
-15	GLN	---	GLN	GLN	GLN	---	---	GLN	GLN	GLN	GLN	GLN	GLN	---	---	GLN	GLN	---
-14	LEU	---	PHE	PHE	PHE	---	---	PHE	VAL	VAL	VAL	VAL	VAL	---	---	PHE	PHE	---
-13	LEU	---	LEU	LEU	PHE	---	---	PHE	PHE	PHE	PHE	PHE	PHE	---	---	PHE	LEU	---
-12	LEU	---	GLY	GLY	GLY	---	---	GLY	ILE	ILE	ILE	ILE	ILE	---	---	GLY	GLY	---
-11	LEU	---	ILE	ILE	ILE	---	---	ILE	PHE	PHE	PHE	PHE	PHE	---	---	ILE	ILE	---
-10	LEU	---	LEU	LEU	LEU	---	---	LEU	LEU	LEU	LEU	LEU	LEU	---	---	LEU	LEU	---
-9	LEU	---	TPP	LEU	LEU	---	---	LEU	LEU	LEU	LEU	LEU	LEU	---	---	LEU	LEU	---
-8	PHE	---	PHE	LEU	LEU	---	---	LEU	LEU	LEU	LEU	LEU	LEU	---	---	LEU	LEU	---
-7	GLY	---	THR	TRP	TRP	---	---	TRP	CYS	CYS	CYS	TRP	CYS	---	---	TRP	TRP	---
-6	ILE	---	VAL	PHE	PHE	---	PHE	PHE	VAL	VAL	VAL	LEU	VAL	---	VAL	PHE	PHE	---
-5	PRO	---	VAL	PRO	PRO	---	PRO	PRO	SER	SER	SER	SER	SER	---	---	PRO	PRO	---
-4	GLY	---	VAL	GLY	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	---	GLY	GLY	---
-3	MET	---	VAL	ILE	ILE	---	ILE	ILE	ALA	ALA	ALA	ALA	VAL	---	---	SER	ILE	---
-2	ILE	---	ARG	LYS	ARG	---	ARG	ARG	HIS	HIS	HIS	HIS	ARG	---	---	ARG	ARG	---
-1	CYS	---	CYS	CYS	CYS	---	CYS	CYS	CYS	GLY	GLY	GLY	GLY	---	---	CYS	CYS	---

SIGNAL PEPTIDES OF MOU:

	124 C.C58 VxSer 'CL	125 WRL- RF28 (VX28) 'CL	126 E225 'CL
-29	---	---	---
-28	---	---	---
-27	---	---	---
-26	---	---	---
-25	---	---	---
-24	---	---	---
-23	---	---	---
-22	---	---	---
-21	---	---	---
-20	MET	MET	ME'
-19	LYS	LYS	GLN
-18	SER	SER	THR
-17	GLN	GLN	HIS
-16	THR	THR	THR
-15	GLN	GLN	GLN
-14	VAL	VAL	VAL
-13	PHE	PHE	PHE
-12	ILE	ILE	VAL
-11	PHE	PHE	TYR
-10	LEU	LEU	ME
-9	LEU	LEU	LEU
-8	LEU	LEU	LEU
-7	CYS	CYS	TRP
-6	VAL	VAL	LEU
-5	SER	SER	SER
-4	GLY	GLY	GLN
-3	ALA	ALA	VAL
-2	HIS	HIS	GLN
-1	GLY	GLY	GLN

	144	145	1
	14.6b.1	26.4.1	5
	CL	CL	7
-29			
-28			
-27			
-26			
-25			
-24			
-23			
-22			
-21	ASP	ASP	
-20	PHE	PHE	
-19	GLN	GLN	
-18	VAL	VAL	
-17	GLN	GLN	
-16	ILE	ILE	
-15	PHE	PHE	
-14	SER	SER	
-13	PHE	PHE	
-12	LEU	LEU	
-11	LEU	LEU	
-10	ILE	ILE	
-9	SER	SER	
-8	ALA	ALA	
-7	SER	SER	
-6	VAL	VAL	
-5	ILE	ILE	
-4	ILE	ILE	
-3	SER	SER	
-2	ARG	ARG	
-1	GLY	GLY	

	168	169	170	171
	4C11	567	10.4	3C
	'CL	'CL	'CL	'C
		↓	↓	↓
-29	---	---	---	
-28	---	---	---	
-27	---	---	---	
-26	---	---	---	
-25	---	---	---	
-24	---	---	---	
-23	---	---	---	
-22	MET	MET		
-21	H15	PHZ		
-20	PHZ	PHZ		
-19	GLN	GLN		
-18	VAL	VAL		
-17	GLN	GLN		
-16	ILE	ILE		II
-15	PHZ	PHZ		PH
-14	SER	SER		
-13	PHZ	PHZ		
-12	LEU	LEU		LE
-11	LEU	LEU		LE
-10	ILE	ILE		LE
-9	SER	SER		SH
-8	ALA	ALA		SH
-7	SER	SER		SH
-6	VAL	VAL		VI
-5	ILE	ILE		VI
-4	MET	ILE		
-3	SER	SER		SH
-2	ARG	ARG		SH
-1				

SIGNAL PEPTIDES OF MOUSE KAPPA LIGHT CHAINS (cont'd)

81	82	83	84
5D3	6G11	37A4	T3C
'CL	'CL	'CL	'CL

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MET      MET
ASP      ASP
PHE      PHE

LEU      GLN
VAL      VAL
GLN      GLN
ILE      ILE
PHE      PHE

SER      SER
PHE      PHE
LEU      LEU
LEU      LEU
ILE      ILE

SER      SER
ALA      ALA
SER      SER
VAL      VAL
ALA      ILE

MET      MET
SER      THR
ARG      ARG
GLY      GLY
          SER
          GLY

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02	103	104	105
'CL	K2A	RFT2	Lym-1
	'CL	'CL	'CL

[illegible]

1	121	122	123
2	BXW-16	K3	C.C58
3	'CL	'CL	M75

T					
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--	MET				
SP	ASP				
ST	ILE				MET
RG-	ARG	---		LYS	
RO	ALA			SER	
LA	PRO	---		GLN	
EN	GLN	MET		THR	
				GLN	
IE	PHE			VAL	
LE	LEU	GLY		TRP	
CE	CYS	ILE		ILE	
EU	ILE	VAL		PHE	
LE	LEU	PHE		LEU	
EU	LEU	THR		LEU	
RO	TRP	PHE		CYS	
HE	PHE	SER		CYS	
RN	ILE	LEU		VAL	
	PRO	VAL		SER	
LY	GLY	ASP		GLY	
AL	ALA	ALA		ALA	
RG-	ARG	ARG		HIS	
YS	CYS	CYS		GLN	

[illegible][illegible][illegible]

SIGNAL PEPTIDES OF MOUSE KAPPA LIGHT CHAINS (cont'd)

	190	191	192	193	194	195	196	197	198	# OF	# OF	OCCURRENCES	VARIABILITY
	K2	40-140	MOPC	19,22.1	2154	1(K0)	5563	42.9	4.14.3	SEQUENCES	AMINO	OF MOST COMMON	
	'CL	'CL	21'CL	'CL	'CL	'CL	(C3H)	E5.2	'CL		ACIDS	AMINO ACID	
-29	---	---	MET	---	---	---	---	---	---	6	2	5(MET)	2.4
-28	---	---	HIS	---	---	---	---	---	---	6	1	6(HIS)	1.
-27	---	---	GLN	---	---	---	---	---	---	6	2	5(GLN)	2.4
-26	---	---	THR	---	---	---	---	---	---	6	3	4(THR)	4.5
-25	---	---	SER	---	---	---	---	---	---	7	3	5(SER)	4.2
-24	---	---	MET	---	---	---	---	---	---	10	3	8(MET)	3.7
-23	---	---	GLY	---	---	---	---	---	---	11	2	10(GLY)	2.2
-22	---	---	ILE	---	---	---	---	---	---	54	4	43(MET)	5.
-21	---	---	LYS	---	---	---	---	---	---	59	5	43(ASP)	5.9
-20	---	---	MET	---	---	---	---	---	---	119	8	75(MET)	13.
-19	---	---	ARG	---	---	---	---	---	---	150	11	35(+)	47.
-18	---	---	THR	---	---	---	---	---	---	153	13	39(VAL)	51.
-17	---	---	PRO	---	---	---	---	---	---	156	9	62(GLN)	23.
-16	---	---	ALA	---	---	---	---	---	---	162	9	46(ILE)	32.
-15	---	---	MET	---	---	---	---	---	---	167	10	60(GLN)	28.
-14	---	---	TRP	---	---	---	---	---	---	171	8	45(SER)	30.
-13	---	---	GLY	---	---	---	---	---	---	177	9	94(LEU)	17.
-12	---	---	PRO	---	---	---	---	---	---	180	11	80(LEU)	25.
-11	---	---	PHE	---	---	---	---	---	---	175	7	82(LEU)	15.
-10	---	---	SER	---	---	---	---	---	---	180	8	117(LEU)	12.
-9	---	---	HIS	---	---	---	---	---	---	182	10	85(LEU)	21.
-8	---	---	PHE	---	---	---	---	---	---	183	11	74(LEU)	27.
-7	---	---	SER	---	---	---	---	---	---	183	9	101(THR)	16.
-6	---	---	ILE	---	---	---	---	---	---	186	9	86(VAL)	19.
-5	---	---	VAL	---	---	---	---	---	---	190	13	71(PRO)	35.
-4	---	---	GLY	---	---	---	---	---	---	189	12	95(GLY)	24.
-3	---	---	ALA	---	---	---	---	---	---	189	8	98(SER)	15.
-2	---	---	ARG	---	---	---	---	---	---	190	13	75(ARG)	33.
-1	---	---	CYS	---	---	---	---	---	---	194	7	121(GLY)	11.

PRECURSOR OF:

- 1) S107A'CL: MOUSE KAPPA I
- 2) 17/9'CL: MOUSE KAPPA LI
- 3) 198.5C2'CL: MOUSE KAPPA
- 4) 198.3D3'CL: MOUSE KAPPA
- 5) 198.5C8'CL: MOUSE KAPPA
- 6) 198.4D9'CL: MOUSE KAPPA
- 7) 180.2G6'CL: MOUSE KAPPA
- 8) 180.6D10'CL: MOUSE KAPPA
- 9) 6A4'CL: MOUSE KAPPA LI
- 10) D23'CL: MOUSE KAPPA LI
- 11) 180.7C9'CL: MOUSE KAPPA
- 12) 180.5G4'CL: MOUSE KAPPA
- 13) TFS-139'CL: MOUSE KAPPA
- 14) 180.2B2'CL: MOUSE KAPPA
- 15) F6-3'CL: MOUSE KAPPA L
- 16) B13B4C8'CL: MOUSE KAPPA
- 17) MRL-1'CL: MOUSE KAPPA L
- 18) MRL-DNA10'CL: MOUSE KA
- 19) K5.1'CL: MOUSE KAPPA L
- 20) BC-1004'CL: MOUSE KAPPA
- 21) B003-46/2D7'CL: MOUSE
- 22) L XIX 27'CL: MOUSE KAP
- 23) 10-25'CL: MOUSE KAPPA
- 24) 5-14'CL: MOUSE KAPPA I
- 25) 9-40'CL: MOUSE KAPPA I
- 26) 12-40'CL: MOUSE KAPPA
- 27) 3-13'CL: MOUSE KAPPA I
- 28) IdB5.7'CL: MOUSE KAPPA
- 29) vk-1A'CL: MOUSE KAPPA
- 30) MOPC-460'CL: MOUSE KAP
- 31) vk-1C'CL: MOUSE KAPPA
- 32) vk-1B'CL: MOUSE KAPPA
- 33) 4-4-20'CL: MOUSE KAPPA
- 34) 3-24'CL: MOUSE KAPPA
- 35) MRL-4'CL: MOUSE KAPPA
- 36) 17C1'CL: MOUSE KAPPA
- 37) 14C3'CL: MOUSE KAPPA
- 38) K1A5'CL: MOUSE KAPPA
- 39) vk-1C'CL: MOUSE KAPPA
- 40) v16-19'CL: MOUSE KAPPA
- 41) 6F8'CL: MOUSE KAPPA L
- 42) 4D4'CL: MOUSE KAPPA L
- 43) K18.1'CL: MOUSE KAPPA
- 44) RP93'CL: MOUSE KAPPA
- 45) 17G5'CL: MOUSE KAPPA
- 46) 36.5.7B'CL: MOUSE KAP
- 47) W3129'CL: MOUSE KAPPA
- 48) 42.4B.12.2'CL: MOUSE
- 49) 42.7B3.2'CL: MOUSE KA
- 50) BKN-14'CL: MOUSE KAPPA
- 51) PaVK24B'CL: MOUSE KAP
- 52) VKAPPA 24B'CL: MOUSE
- 53) VK-25-39'CL: MOUSE KA
- 54) VK-25-47'CL: MOUSE KA
- 55) PaVK24.2'CL: MOUSE KA
- 56) PaVK24.1'CL: MOUSE KA
- 57) PaVK24A'CL: MOUSE KAP
- 58) PaVK24C'CL: MOUSE KAP
- 59) MOPC167'CL: MOUSE KAP
- 60) VKAPPA167'CL: MOUSE K
- 61) VKAPPA 24A'CL: MOUSE
- 62) MOPC11'CL: MOUSE KAPPA
- 63) MOPC321'CL: MOUSE KAPPA
- 64) 2.7.1G.10'CL: MOUSE K
- 65) vk-21C'CL: MOUSE KAPPA
- 66) vk-21A'CL: MOUSE KAPPA
- 67) 05'CL: MOUSE KAPPA LI
- 68) 11'CL: MOUSE KAPPA LI
- 69) 12'CL: MOUSE KAPPA LI
- 70) 4.3.6F8'CL: MOUSE KAP
- 71) MOPC63'CL: MOUSE KAPPA L
- 72) 13'CL: MOUSE KAPPA LI
- 73) 30'CL: MOUSE KAPPA LI
- 74) 2B2'CL: MOUSE KAPPA L
- 75) 12C4'CL: MOUSE KAPPA
- 76) MRL-B1stone7'CL: MOUS
- 77) 7B6'CL: MOUSE KAPPA L
- 78) MRL-22'CL: MOUSE KAPPA
- 79) VABE8'CL: MOUSE KAPPA
- 80) 18-2-3'CL: MOUSE KAPPA
- 81) 5D3'CL: MOUSE KAPPA I
- 82) 6G11'CL: MOUSE KAPPA
- 83) 37A4'CL: MOUSE KAPPA
- 84) T3C'CL: MOUSE KAPPA I
- 85) L8'CL: MOUSE KAPPA LI
- 86) S107B'CL: MOUSE KAPPA
- 87) T2E(1)'CL: MOUSE KAPPA
- 88) 38CV3'CL: MOUSE KAPPA
- 89) 38CV4'CL: MOUSE KAPPA
- 90) V-K10 ARS-A'CL: MOUSE
- 91) AC-1001'CL: MOUSE KAP
- 92) 7F11'CL: MOUSE KAPPA
- 93) 2H1'CL: MOUSE KAPPA I
- 94) H12'CL: MOUSE KAPPA I
- 95) 5-27'CL: MOUSE KAPPA
- 96) 18C10'CL: MOUSE KAPPA
- 97) 38C13'CL: MOUSE KAPPA
- 98) 38C'CL: MOUSE KAPPA I
- 99) PC613'CL: MOUSE KAPPA
- 100) 38C13V'CL: MOUSE KAPPA
- 101) MOPC173B'CL: MOUSE KA
- 102) T1'CL: MOUSE KAPPA LI
- 103) K2A'CL: MOUSE KAPPA I

PRECURSOR OF:

- 1) S107A'CL: MOUSE KAPPA LIGHT CHAINS I
- 2) 17/9'CL: MOUSE KAPPA LIGHT CHAINS I
- 3) 198.5C2'CL: MOUSE KAPPA LIGHT CHAINS I
- 4) 198.3D3'CL: MOUSE KAPPA LIGHT CHAINS I
- 5) 198.5C8'CL: MOUSE KAPPA LIGHT CHAINS I
- 6) 198.4D9'CL: MOUSE KAPPA LIGHT CHAINS I
- 7) 180.2G6'CL: MOUSE KAPPA LIGHT CHAINS I
- 8) 180.6D10'CL: MOUSE KAPPA LIGHT CHAINS I
- 9) 6A4'CL: MOUSE KAPPA LIGHT CHAINS I
- 10) D23'CL: MOUSE KAPPA LIGHT CHAINS I
- 11) 180.7C9'CL: MOUSE KAPPA LIGHT CHAINS I
- 12) 180.5G4'CL: MOUSE KAPPA LIGHT CHAINS I
- 13) T75-139'CL: MOUSE KAPPA LIGHT CHAINS I
- 14) 180.2B2'CL: MOUSE KAPPA LIGHT CHAINS I
- 15) F6-3'CL: MOUSE KAPPA LIGHT CHAINS I
- 16) B13H4C9'CL: MOUSE KAPPA LIGHT CHAINS I
- 17) MBR1'CL: MOUSE KAPPA LIGHT CHAINS I
- 18) MRL-DNA10'CL: MOUSE KAPPA LIGHT CHAINS II
- 19) K5.1'CL: MOUSE KAPPA LIGHT CHAINS II
- 20) BC-1004'CL: MOUSE KAPPA LIGHT CHAINS II
- 21) B003-46/2D7'CL: MOUSE KAPPA LIGHT CHAINS II
- 22) L XIX 27'CL: MOUSE KAPPA LIGHT CHAINS II
- 23) 10-25'CL: MOUSE KAPPA LIGHT CHAINS II
- 24) 5-14'CL: MOUSE KAPPA LIGHT CHAINS II
- 25) 9-40'CL: MOUSE KAPPA LIGHT CHAINS II
- 26) 12-40'CL: MOUSE KAPPA LIGHT CHAINS II
- 27) 3-13'CL: MOUSE KAPPA LIGHT CHAINS II
- 28) IdB5.7'CL: MOUSE KAPPA LIGHT CHAINS II
- 29) vk-1A'CL: MOUSE KAPPA LIGHT CHAINS II
- 30) MOPC-460'CL: MOUSE KAPPA LIGHT CHAINS II
- 31) vk-1C'CL: MOUSE KAPPA LIGHT CHAINS II
- 32) vk-1B'CL: MOUSE KAPPA LIGHT CHAINS II
- 33) 4-4-20'CL: MOUSE KAPPA LIGHT CHAINS II
- 34) 3-24'CL: MOUSE KAPPA LIGHT CHAINS II
- 35) MRL-4'CL: MOUSE KAPPA LIGHT CHAINS II
- 36) 17C1'CL: MOUSE KAPPA LIGHT CHAINS II
- 37) 14C3'CL: MOUSE KAPPA LIGHT CHAINS II
- 38) K1A5'CL: MOUSE KAPPA LIGHT CHAINS II
- 39) vk-1C'CL: MOUSE KAPPA LIGHT CHAINS II
- 40) v16-19'CL: MOUSE KAPPA LIGHT CHAINS II
- 41) 6F8'CL: MOUSE KAPPA LIGHT CHAINS II
- 42) 4D4'CL: MOUSE KAPPA LIGHT CHAINS II
- 43) K18.1'CL: MOUSE KAPPA LIGHT CHAINS II
- 44) RP93'CL: MOUSE KAPPA LIGHT CHAINS II
- 45) 17G5'CL: MOUSE KAPPA LIGHT CHAINS II
- 46) 36.5.7B'CL: MOUSE KAPPA LIGHT CHAINS II
- 47) W3129'CL: MOUSE KAPPA LIGHT CHAINS II
- 48) 42.4B.12.2'CL: MOUSE KAPPA LIGHT CHAINS II
- 49) 42.7B3.2'CL: MOUSE KAPPA LIGHT CHAINS II
- 50) BXM-14'CL: MOUSE KAPPA LIGHT CHAINS II
- 51) PaVK24B'CL: MOUSE KAPPA LIGHT CHAINS II
- 52) VKAPPA 24B'CL: MOUSE KAPPA LIGHT CHAINS II
- 53) VK-25-39'CL: MOUSE KAPPA LIGHT CHAINS II
- 54) VK-25-47'CL: MOUSE KAPPA LIGHT CHAINS II
- 55) PaVK24.2'CL: MOUSE KAPPA LIGHT CHAINS II
- 56) PaVK24.1'CL: MOUSE KAPPA LIGHT CHAINS II
- 57) PaVK24A'CL: MOUSE KAPPA LIGHT CHAINS II
- 58) PaVK24C'CL: MOUSE KAPPA LIGHT CHAINS II
- 59) MOPC167'CL: MOUSE KAPPA LIGHT CHAINS II
- 60) VKAPPA167'CL: MOUSE KAPPA LIGHT CHAINS II
- 61) VKAPPA 24A'CL: MOUSE KAPPA LIGHT CHAINS II
- 62) MOPC11'CL: MOUSE KAPPA LIGHT CHAINS III
- 63) MOPC321'CL: MOUSE KAPPA LIGHT CHAINS III
- 64) 2.7.1G.10'CL: MOUSE KAPPA LIGHT CHAINS III
- 65) VK-21G'CL: MOUSE KAPPA LIGHT CHAINS III
- 66) VK-21A'CL: MOUSE KAPPA LIGHT CHAINS III
- 67) 05'CL: MOUSE KAPPA LIGHT CHAINS III
- 68) 11'CL: MOUSE KAPPA LIGHT CHAINS III
- 69) 12'CL: MOUSE KAPPA LIGHT CHAINS III
- 70) 4.3.6F8'CL: MOUSE KAPPA LIGHT CHAINS III
- 71) MOPC63'CL: MOUSE KAPPA LIGHT CHAINS III
- 72) 13'CL: MOUSE KAPPA LIGHT CHAINS III
- 73) 30'CL: MOUSE KAPPA LIGHT CHAINS III
- 74) 2B2'CL: MOUSE KAPPA LIGHT CHAINS IV
- 75) 12C4'CL: MOUSE KAPPA LIGHT CHAINS IV
- 76) MRL-Histone7'CL: MOUSE KAPPA LIGHT CHAINS IV
- 77) 7B6'CL: MOUSE KAPPA LIGHT CHAINS IV
- 78) MRL-22'CL: MOUSE KAPPA LIGHT CHAINS IV
- 79) VAREB'CL: MOUSE KAPPA LIGHT CHAINS IV
- 80) 18-2-3'CL: MOUSE KAPPA LIGHT CHAINS IV
- 81) 5D3'CL: MOUSE KAPPA LIGHT CHAINS IV
- 82) 6G11'CL: MOUSE KAPPA LIGHT CHAINS IV
- 83) 37A4'CL: MOUSE KAPPA LIGHT CHAINS IV
- 84) T3C'CL: MOUSE KAPPA LIGHT CHAINS IV
- 85) L8'CL: MOUSE KAPPA LIGHT CHAINS IV
- 86) S107B'CL: MOUSE KAPPA LIGHT CHAINS IV
- 87) T2E(1)'CL: MOUSE KAPPA LIGHT CHAINS IV
- 88) 38CV3'CL: MOUSE KAPPA LIGHT CHAINS IV
- 89) 38CV4'CL: MOUSE KAPPA LIGHT CHAINS IV
- 90) V-K10 ARS-A'CL: MOUSE KAPPA LIGHT CHAINS V
- 91) AC-1001'CL: MOUSE KAPPA LIGHT CHAINS V
- 92) 7F11'CL: MOUSE KAPPA LIGHT CHAINS V
- 93) 2H1'CL: MOUSE KAPPA LIGHT CHAINS V
- 94) H12'CL: MOUSE KAPPA LIGHT CHAINS V
- 95) 5-27'CL: MOUSE KAPPA LIGHT CHAINS V
- 96) 18C10'CL: MOUSE KAPPA LIGHT CHAINS V
- 97) 38C13'CL: MOUSE KAPPA LIGHT CHAINS V
- 98) 38C'CL: MOUSE KAPPA LIGHT CHAINS V
- 99) PC613'CL: MOUSE KAPPA LIGHT CHAINS V
- 100) 38C13V'CL: MOUSE KAPPA LIGHT CHAINS V
- 101) MOPC173B'CL: MOUSE KAPPA LIGHT CHAINS V
- 102) T1'CL: MOUSE KAPPA LIGHT CHAINS V
- 103) K2A'CL: MOUSE KAPPA LIGHT CHAINS V

PRECURSOR OF: (cont'd)

- 104) RPT2'CL: MOUSE KAPPA LIGHT CHAINS V
 105) Lym-1'CL: MOUSE KAPPA LIGHT CHAINS V
 106) VK33'CL: MOUSE KAPPA LIGHT CHAINS V
 107) 10.2.8'CL: MOUSE KAPPA LIGHT CHAINS V
 108) VT1/B'CL: MOUSE KAPPA LIGHT CHAINS V
 109) L6'CL: MOUSE KAPPA LIGHT CHAINS V
 110) 2-2G4'CL: MOUSE KAPPA LIGHT CHAINS V
 111) 2-2C8'CL: MOUSE KAPPA LIGHT CHAINS V
 112) B16.2K1'CL: MOUSE KAPPA LIGHT CHAINS V
 113) UN34.11'CL: MOUSE KAPPA LIGHT CHAINS V
 114) C.AKR'CL: MOUSE KAPPA LIGHT CHAINS V
 115) 9F/CAME1'CL: MOUSE KAPPA LIGHT CHAINS V
 116) PERA/EI'CL: MOUSE KAPPA LIGHT CHAINS V
 117) 4.2.6D12'CL: MOUSE KAPPA LIGHT CHAINS V
 118) SK/CAMRk'CL: MOUSE KAPPA LIGHT CHAINS V
 119) C8.5V'CL: MOUSE KAPPA LIGHT CHAINS V
 120) UN42.5'CL: MOUSE KAPPA LIGHT CHAINS V
 121) BXM-16'CL: MOUSE KAPPA LIGHT CHAINS V
 122) K3'CL: MOUSE KAPPA LIGHT CHAINS V
 123) C.C58 M75'CL: MOUSE KAPPA LIGHT CHAINS V
 124) C.C58 VK8e'CL: MOUSE KAPPA LIGHT CHAINS V
 125) MRL-RF28(VK28)'CL: MOUSE KAPPA LIGHT CHAINS V
 126) E225'CL: MOUSE KAPPA LIGHT CHAINS V
 127) MFC11: MOUSE KAPPA LIGHT CHAINS V
 128) A003=40/SG7'CL: MOUSE KAPPA LIGHT CHAINS V
 129) CEA 66-E3'CL: MOUSE KAPPA LIGHT CHAINS V
 130) VTNP'CL: MOUSE KAPPA LIGHT CHAINS V
 131) CEM231.6.7'CL: MOUSE KAPPA LIGHT CHAINS V
 132) BALB/cVK8e'CL: MOUSE KAPPA LIGHT CHAINS V
 133) B6.2'CL: MOUSE KAPPA LIGHT CHAINS V
 134) MOPC21: MOUSE KAPPA LIGHT CHAINS V
 135) 17-1A'CL: MOUSE KAPPA LIGHT CHAINS V
 136) E7'CL: MOUSE KAPPA LIGHT CHAINS V
 137) MRL-RF24'CL: MOUSE KAPPA LIGHT CHAINS V
 138) L7'CL: MOUSE KAPPA LIGHT CHAINS V
 139) T2'CL: MOUSE KAPPA LIGHT CHAINS V
 140) 87.92.6'CL: MOUSE KAPPA LIGHT CHAINS V
 141) 45.21.1'CL: MOUSE KAPPA LIGHT CHAINS VI
 142) 10C11'CL: MOUSE KAPPA LIGHT CHAINS VI
 143) 18G8'CL: MOUSE KAPPA LIGHT CHAINS VI
 144) 14.6b.1'CL: MOUSE KAPPA LIGHT CHAINS VI
 145) 26.4.1'CL: MOUSE KAPPA LIGHT CHAINS VI
 146) 5G11'CL: MOUSE KAPPA LIGHT CHAINS VI
 147) 14B4'CL: MOUSE KAPPA LIGHT CHAINS VI
 148) 58.2C.10.3'CL: MOUSE KAPPA LIGHT CHAINS VI
 149) 6B10'CL: MOUSE KAPPA LIGHT CHAINS VI
 150) 4F10'CL: MOUSE KAPPA LIGHT CHAINS VI
 151) 6F6'CL: MOUSE KAPPA LIGHT CHAINS VI
 152) 7C6'CL: MOUSE KAPPA LIGHT CHAINS VI
 153) 8E3'CL: MOUSE KAPPA LIGHT CHAINS VI
 154) H26'CL: MOUSE KAPPA LIGHT CHAINS VI
 155) 3F2'CL: MOUSE KAPPA LIGHT CHAINS VI
 156) 12G10'CL: MOUSE KAPPA LIGHT CHAINS VI
 157) 10G10'CL: MOUSE KAPPA LIGHT CHAINS VI
 158) 3E3'CL: MOUSE KAPPA LIGHT CHAINS VI
 159) 13D4'CL: MOUSE KAPPA LIGHT CHAINS VI
 160) 9G6'CL: MOUSE KAPPA LIGHT CHAINS VI
 161) 3B6'CL: MOUSE KAPPA LIGHT CHAINS VI
 162) 11G3'CL: MOUSE KAPPA LIGHT CHAINS VI
 163) 564'CL: MOUSE KAPPA LIGHT CHAINS VI
 164) 550'CL: MOUSE KAPPA LIGHT CHAINS VI
 165) 563'CL: MOUSE KAPPA LIGHT CHAINS VI
 166) 42.5D4.2'CL: MOUSE KAPPA LIGHT CHAINS VI
 167) 37.1B5.2'CL: MOUSE KAPPA LIGHT CHAINS VI
 168) 4C11'CL: MOUSE KAPPA LIGHT CHAINS VI
 169) 567'CL: MOUSE KAPPA LIGHT CHAINS VI
 170) 10.4'CL: MOUSE KAPPA LIGHT CHAINS VI
 171) 3C5'CL: MOUSE KAPPA LIGHT CHAINS VI
 172) 5G2'CL: MOUSE KAPPA LIGHT CHAINS VI
 173) 70Z/3'CL: MOUSE KAPPA LIGHT CHAINS VI
 174) 2H7'CL: MOUSE KAPPA LIGHT CHAINS VI
 175) L6'CL: MOUSE KAPPA LIGHT CHAINS VI
 176) 2C7'CL: MOUSE KAPPA LIGHT CHAINS VI
 177) 38CV1'CL: MOUSE KAPPA LIGHT CHAINS VI
 180) MFC11C: MOUSE KAPPA LIGHT CHAIN OF A VARIANT PROTEIN MADE BY CLONED MFC11 WITH THE VARIABLE REGION DELETED
 186) 91A3'CL: MOUSE KAPPA LIGHT CHAIN
 187) MOPC41'CL: MOUSE KAPPA LIGHT CHAIN
 188) MOPC41A: MOUSE KAPPA LIGHT CHAIN OF MOPC41 (2 DIFFERENT PRECURSORS)
 189) MOPC41B: MOUSE KAPPA LIGHT CHAIN OF MOPC41 (2 DIFFERENT PRECURSORS)
 190) K2'CL: MOUSE KAPPA LIGHT CHAIN OF K2'CL
 191) 40-140'CL: MOUSE KAPPA LIGHT CHAIN
 192) MOPC21'CL: MOUSE KAPPA LIGHT CHAIN
 193) 19.22.1'CL: MOUSE KAPPA LIGHT CHAIN

REFERENCE: SIGNAL PEPTIDES OF MOUSE KAPPA LIGHT CHAINS

- 1) S107A'CL: KWAN, S.P., RUDIKOFF, S., SEIDMAN, J.G., LEDER, P. & SCHARFF, M.D. (1981) J. EXP. MED., 153, 1366-1370.
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- 196) 5563(C38)L: SINGER, H.H. AUTHOR 11/06/81
- 197) 42.9B5.2'CL: WANG, D., L.
- 198) 4.14.3'CL: WANG, D., LIAO

GENERAL NOTES: SIGNAL P

THE NUCLEOTIDE SEQUENCE OF THE SPLICING OUT OF THESE T HOWEVER, IF THE SPLICING RE OCCURRING WITHIN THE CODON

CLONE:	SOU
HK100'CL	HUM
HK101'CL	HUM
HK102'CL	HUM
MOPC173B'CL	MOU
S107B'CL	MOU
L8'CL	MOU
K2'CL	MOU
MPC11'CL	MOU
VKAPPA167'CL	MOU
L6'CL	MOU
L7'CL	MOU
T1'CL	MOU
T2'CL	MOU
VT1/B'CL	MOU
VTNP'CL	MOU

SPECIFIC NOTES: SIGNAL

- 13) TF5-139'CL: FROM BALB.
- 17) MB1'CL: IT IS A CHIM (IGG1-KAPPA).
- 19) K5.1'CL: ISOLATED BY :
- 38) K1A5'CL: ISOLATED BY :
- 43) K18.1'CL: ISOLATED BY :
- 44) RP93'CL: IT WAS ISOLA
- 60) VKAPPA167'CL: THE V I
- 64) 2.7.10.10'CL: A MOUSE SAME AFFINITY
- 67) 05'CL: PATHOGENIC AUT
- 68) 11'CL: PATHOGENIC AUT
- 69) 12'CL: PATHOGENIC AUT
- 72) 13'CL: PATHOGENIC AUT
- 73) 30'CL: PATHOGENIC AUT
- 74) 2B2'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 75) 12C4'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 77) 7B6'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 82) 6G11'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 84) T3C'CL: ANTI-IDIOTYPE TO RE-REARRANG
- 85) L8'CL: THE SPLICING
- 86) 8107B'CL: THE SPLICI
- 87) T2E(1)'CL: ANTI-IDIOT DUE TO RE-REAN
- 90) V-K10 ARS-A'CL: TERMI
- 93) 2B1'CL: A CHIMERIC AN
- 100) 38C13V'CL: ANTI-IDIOT DUE TO RE-REAN
- 104) RPT2'CL: THE VARIABLE KAPPA AND IGG1 CH22: SO2 214
- 126) E225'CL: IT REACTS WIT
- 127) MFC11: THE TRANSLATED
- 129) CEA 66-83'CL: THIS AN
- 131) CEM231.6.7'CL: IT IS I
- 133) B6.2'CL: THE V-REGION
- 138) L7'CL: THE AUTHORS SI NO RESIDUES A
- 140) 87.92.6'CL: MONOCLONAL THE MAMMALIAN REOVIRUS TYPE
- 142) 10C11'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 143) 18G8'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 146) 5G11'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 147) 14B4'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 149) 6B10'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 150) 4F10'CL: THE SEQUENCE 1 AFTER IMMUNIZ
- 154) H26'CL: ISOLATED 7 DA
- 155) 3F2'CL: ISOLATED 7 DA

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- 12/21/82
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- 193) 19.22.1'CL: AKOLKAR, P.N., SIKDER, S.K., BHATTACHARYA, S.B., LIAO, J., GRUEZO, F., MORRISON, S.L. & KABAT, E.A. (1987) J. IMMUNOL., 138, 4472-4479. ERRATA CORRECTED 139, 3911.
- 194) 2154'CL: KELLEY, D.E., WIEDEMANN, L.M., PITTET, A.-C., STRAUSS, S., NELSON, K.J., DAVIS, J., VAN NESS, B. & PERRY, R.P. (1985) MOLEC. & CELL. BIOL., 5, 7, 1660-1675.
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GENERAL NOTES: SIGNAL PEPTIDES OF MOUSE KAPPA LIGHT CHAINS

THE NUCLEOTIDE SEQUENCES OF DIFFERENT CLONES CONTAIN AN INTERVENING SEQUENCE OF NONTRANSLATED BASES OF VARYING LENGTHS. THE SPLICING OUT OF THESE INTRONS COULD OCCUR BETWEEN AMINO ACID POSITIONS -3 AND -4, OR -4 AND -3, OR WITHIN POSITION -4. HOWEVER, IF THE SPLICING REQUIRES GT AT THE 5'-END AND AG AT THE 3'-END OF THE INTRON, THIS WOULD DEFINE THE JOINING AS OCCURRING WITHIN THE CODON OF AMINO ACID RESIDUE -4. THE INTRON SIZES OF DIFFERENT SEQUENCES ARE LISTED BELOW:

CLONE:	SOURCE:	INTRON SIZE:
HK100'CL	HUMAN FETAL LIVER DNA	118
HK101'CL	HUMAN FETAL LIVER DNA	125
HK102'CL	HUMAN FETAL LIVER DNA	125
MOPC173B'CL	MOUSE ADULT DNA	121
S107B'CL	MOUSE ADULT MYELOMA DNA	175
L8'CL	MOUSE ADULT LIVER DNA	175
K2'CL	MOUSE EMBRYO DNA	118
MPC11'CL	MOUSE ADULT DNA	242
VKAPPA167'CL	MOUSE ADULT LIVER DNA	365
L6'CL	MOUSE ADULT LIVER DNA	113
L7'CL	MOUSE ADULT LIVER DNA	206
T1'CL	MOUSE ADULT MYELOMA DNA	113
T2'CL	MOUSE ADULT MYELOMA DNA	215
VT1/B'CL	MOUSE ADULT MYELOMA DNA	113
VTN'B'CL	MOUSE HYBRIDOMA DNA	177

SPECIFIC NOTES: SIGNAL PEPTIDES OF MOUSE KAPPA LIGHT CHAINS

- 13) TF5-139'CL: FROM BALB/c NEONATAL SPLEEN CELLS.
- 17) MB1'CL: IT IS A CHIMERIC ANTIBODY WITH MOUSE VARIABLE REGIONS (FROM IGM-KAPPA) AND HUMAN CONSTANT REGIONS (FROM IGG1-KAPPA).
- 19) K5.1'CL: ISOLATED BY STRONG HYBRIDIZATION TO VK-GAT-SPECIFIC PROBES.
- 38) KIA5'CL: ISOLATED BY STRONG HYBRIDIZATION TO VK-GAT-SPECIFIC PROBES.
- 43) K18.1'CL: ISOLATED BY STRONG HYBRIDIZATION TO VK-GAT-SPECIFIC PROBES.
- 44) RP93'CL: IT WAS ISOLATED FROM A BALB/c MOUSE HYPERIMMUNIZED WITH PC-KLH.
- 60) VKAPPA167'CL: THE V REGION IS CALLED VKAPPA24'CL. SEE NOTES OF MOUSE KAPPA LIGHT CHAIN TABLE.
- 64) 2.7.1G.10'CL: A MOUSE-HUMAN CHIMERIC ANTIBODY CONSISTING OF MOUSE VARIABLE REGIONS AND HUMAN CONSTANT REGIONS HAS THE SAME AFFINITY FOR ANTIGEN AS THE ORIGINAL MOUSE ANTIBODY.
- 67) 05'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
- 68) 11'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
- 69) 12'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
- 72) 13'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
- 73) 30'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
- 74) 2B2'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 75) 12C4'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 77) 7B6'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 82) 6G11'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 84) T3C'CL: ANTI-IDIOTYPE ANTIBODY-RESISTANT VARIANT CELL LINE DERIVED FROM B CELL LYMPHOMA 38C13. TUMOR CELL ESCAPE DUE TO RE-REARRANGEMENT OF THE 38C13 TUMOR CELL IGHKAPPA LOCUS.
- 85) L8'CL: THE SPLICING OUT OF THE INTRON OCCURS AT POSITION -6 INSTEAD OF THE USUAL POSITION -4.
- 86) S107B'CL: THE SPLICING OUT OF THE INTRON OCCURS AT POSITION -6 INSTEAD OF THE USUAL POSITION -4.
- 87) T2E(1)'CL: ANTI-IDIOTYPE ANTIBODY-RESISTANT VARIANT CELL LINE DERIVED FROM B CELL LYMPHOMA 38C13. TUMOR CELL ESCAPE DUE TO RE-REARRANGEMENT OF THE 38C13 TUMOR CELL IGHKAPPA LOCUS.
- 90) V-K10 ARS-A'CL: TERMINATION CODON AT POSITION -13.
- 93) 2H1'CL: A CHIMERIC ANTIBODY IS CONSTRUCTED FROM THE MOUSE V-REGION AND HUMAN C-KAPPA REGION.
- 100) 38C13V'CL: ANTI-IDIOTYPE ANTIBODY-RESISTANT VARIANT CELL LINE DERIVED FROM B CELL LYMPHOMA 38C13. TUMOR CELL ESCAPE DUE TO RE-REARRANGEMENT OF THE 38C13 TUMOR CELL IGHKAPPA LOCUS.
- 104) RT2'CL: THE VARIABLE REGIONS OF LIGHT AND HEAVY CHAINS OF THIS HYBRIDOMA HAS BEEN JOINED TO CONSTANT REGIONS OF HUMAN KAPPA AND IGG1 (ENCODING ALLOTYPE RGA1(2) AND RGA1(4) TO FORM A CHIMERIC ANTI-LYMPHOCYTE MONOCLONAL ANTIBODY, CH22, SDZ 214-360. RT2 AND CH22 SHOWED IDENTICAL TISSUE REACTIVITY.
- 126) E225'CL: IT REACTS WITH A PRIVATE IDIOTYPE OF THE ANTI-LYSOZYME ANTIBODY D1.3.
- 127) MPC11: THE TRANSLATED AMINO ACID SEQUENCE FROM NUCLEOTIDE SEQUENCE OF MPC11 AGREES WITH THIS.
- 129) CEA 66-E3'CL: THIS ANTIBODY IS SYNTHESIZED IN ESCHERICHIA COLI.
- 131) CMO231.6.7'CL: IT IS A MOUSE/HUMAN CHIMERIC ANTIBODY WITH MOUSE VARIABLE REGION AND HUMAN IGG1-KAPPA CONSTANT REGION.
- 133) B6.2'CL: THE V-REGIONS WERE USED TO CONSTRUCT A MURINE/HUMAN CHIMERIC ANTIBODY.
- 138) L7'CL: THE AUTHORS SUGGESTED THAT IT IS ALSO POSSIBLE TO SPLICED AT A DIFFERENT POSITION TO GIVE GLY AT POSITION -4 AND NO RESIDUES AT POSITIONS -3 TO -1.
- 140) 87.92.6'CL: MONOCLONAL ANTI-IDIOTYPE ANTIBODY AGAINST THE 9B.G5 ANTIBODY SPECIFIC FOR THE VIRUS NEUTRALIZING EPITOPE ON THE MAMMALIAN REOVIRUS TYPE 3 HEMAGGLUTININ. IT EXPRESSES AN INTERNAL IMAGE OF THE RECEPTOR BINDING EPITOPE OF REOVIRUS TYPE 3, AND ALSO HAS AUTOIMMUNE REACTIVITY TO THE CELL SURFACE RECEPTOR OF REOVIRUS.
- 142) 10C11'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 143) 18GB'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 146) 5G11'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 147) 14B4'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 149) 6B10'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 150) 4F10'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
- 154) B26'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.
- 155) JF2'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.

SPECIFIC NOTES: SIGNAL PEPTIDES OF MOUSE KAPPA LIGHT CHAINS (cont'd)

- 156) 12G10'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.
 157) 10C10'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.
 158) 3E3'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.
 159) 13D4'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.
 160) 9G6'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.
 161) 3B6'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.
 162) 11G3'CL: ISOLATED 7 DAYS AFTER PRIMARY IMMUNIZATION.
 163) 564'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
 164) 550'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
 165) 563'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
 169) 567'CL: PATHOGENIC AUTOANTIBODY PRODUCED BY NEPHRITIS PRONE (SWR X NZB)F1 (SNF1) MOUSE.
 170) 10.4'CL: ANTI-IDIOTYPE ANTIBODY-RESISTANT VARIANT CELL LINE DERIVED FROM B CELL LYMPHOMA 38C13. TUMOR CELL ESCAPE DUE TO RE-REARRANGEMENT OF THE 38C13 TUMOR CELL IgKAPPA LOCUS.
 171) 3C5'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
 174) 2H7'CL: 2H7'CL IS A MOUSE ANTIBODY WHOSE VARIABLE REGIONS HAVE BEEN JOINED TO HUMAN IGG1 AND KAPPA CONSTANT REGIONS. THE RESULTING CHIMERIC MONOCLONAL ANTIBODY HAS STRONG ANTIBODY-DEPENDENT CELLULAR CYTOTOXICITY WITH HUMAN EFFECTOR CELLS AND COMPLEMENT-DEPENDENT CYTOTOXICITY WITH HUMAN COMPLEMENT.
 176) 2C7'CL: THE SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF MRNA OF HYBRIDOMA FROM ADULT MOUSE 7 DAYS AFTER IMMUNIZATION.
 180) MPC11C: THIS SEGMENT IS CONNECTED DIRECTLY TO THE KAPPA LIGHT CHAIN CONSTANT REGION.
 186) 91A3'CL: TERMINATION CODON AT POSITION -13.
 188) MPC41A: THE AMINO ACID SEQUENCE TRANSLATED FROM THE DNA SEQUENCE (SEIDMAN, J.G., MAX, E.E. & LEDER, P. (1979) NATURE, 280, 370-375.) HAS GLU AT POSITION -5.

* THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
-19	(MET, GLN)

SIGNAL PEPTIDES OF MOUSE LAMBDA L

INVARIANT RESIDUES	1 MOPC 104E	2 KL.SJA 83.12 CL	3 RPC 20	4 IG 3C LAMBDA 'CL
-21	MET	MET	MET	MET
-20	ALA	ALA	ALA	ALA
-19	TRP	TRP	TRP	TRP
-18	ILE	ILE	ILE	ILE
-17	---	---	---	---
-16	LEU	SER	SER	SER
-15	---	LEU	LEU	LEU
-14	---	ILE	ILE	ILE
-13	---	LEU	LEU	LEU
-12	---	SER	SER	SER
-11	---	LEU	LEU	LEU
-10	---	LEU	LEU	LEU
-9	---	ALA	ALA	ALA
-8	---	LEU	LEU	LEU
-7	---	---	---	---
-6	---	SER	SER	SER
-5	GLY	SER	SER	SER
-4	---	ALA	ALA	ALA
-3	---	ILE	ILE	ILE
-2	---	SER	SER	SER
-1	---	---	---	---

VARIABILITY

-21	1.
-20	1.
-19	1.
-18	1.
-17	3.4
-16	2.2
-15	1.
-14	2.2
-13	2.2
-12	2.2
-11	---
-10	2.2
-9	2.2
-8	2.2
-7	---
-6	3.4
-5	1.
-4	1.
-3	2.2
-2	4.5
-1	1.

SIGNAL PEPTIDES OF MOUSE LAMBDA LIGHT CHAINS

	INVARIANT RESIDUES	1 MOPC 104E	2 KL SJA 83.12 'CL	3 RPC 20	4 IG 303 LAMBDA 'CL	5 IG 99 LAMBDA 'CL	6 S43 MOPC 'CL	7 MOPC 315	8 WES- IG13 'CL	9 SPE VL 'CL	10 Y31 'CL	11 HOPC -1'CL	12 MOPC 315-26 'CL	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID
-21														12	1	12 (MET)
-20	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	12	1	12 (ALA)
-19	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	12	1	12 (TRP)
-18	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	12	2	7 (ILE)
-17		ILE	ILE	ILE	ILE	ILE	ILE	THR	THR	THR	THR	ILE	THR	12	2	11 (SER)
-16		SER	SER	SER	SER	SER	SER	SER	SER	SER	PRO	SER	SER	12	2	12 (LEU)
-15	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	12	1	11 (ILE)
-14		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	PHE	ILE	ILE	12	2	11 (LEU)
-13		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	PHE	LEU	LEU	12	2	11 (SER)
-12		SER	SER	SER	SER	SER	SER	SER	SER	SER	PHE	SER	SER	12		
-11														12	2	11 (LEU)
-10		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	PHE	LEU	LEU	12	2	11 (LEU)
-9		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	VAL	LEU	LEU	12	2	11 (ALA)
-8		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	LEU	ALA	ALA	12	2	11 (LEU)
-7		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	HIS	LEU	LEU	12		
-6		SER	SER	SER	SER	SER	SER	CYS	CYS	CYS	CYS	SER	CYS	12	2	7 (SER)
-5	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	12	1	12 (SER)
-4	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	12	1	12 (GLY)
-3		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	SER	ALA	ALA	12	2	11 (ALA)
-2		ILE	ILE	ILE	ILE	ILE	ILE	SER	SER	ILE	PHE	ILE	SER	12	3	8 (ILE)
-1	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	12	1	12 (SER)

TUMOR CELL ESCAPE DUE

4 ADULT MOUSE 7 DAYS

4 CONSTANT REGIONS.
ICITY WITH HUMAN

4 ADULT MOUSE 7 DAYS

P. (1979) NATURE, 280,

VARIABILITY

-21	
-20	1.
-19	1.
-18	1.
-17	3.4
-16	2.2
-15	1.
-14	2.2
-13	2.2
-12	2.2
-11	2.2
-10	2.2
-9	2.2
-8	2.2
-7	2.2
-6	3.4
-5	1.
-4	1.
-3	2.2
-2	4.5
-1	1.

REFERENCE: SIGNAL PEPTIDES OF MOUSE LAMBDA LIGHT CHAINS

- 1) MOPC104E: BURSTEIN, Y. & SCHECHTER, I. (1977) PROC. NAT. ACAD. SCI. USA, 74, 716-720. (CHECKED BY AUTHOR)
- 2) KL. S. J. 83. 12' CL: WEISS, S., LEHMANN, K. & COHN, M. (1985) EUR. J. IMMUNOL., 15, 768-772.
- 3) RPC20: BURSTEIN, Y. & SCHECHTER, I. (1978) BIOCHEMISTRY, 17, 2392-2400. (CHECKED BY AUTHOR)
- 4) IG 303LAMBDA' CL: BERNARD, O., HOZUMI, N. & TONEGAWA, S. (1978) CELL, 15, 1133-1144. (CHECKED BY AUTHOR 08/06/79)
- 5) IG 99LAMBDA' CL: BERNARD, O., HOZUMI, N. & TONEGAWA, S. (1978) CELL, 15, 1133-1144. (CHECKED BY AUTHOR 08/06/79)
- 6) S43' CL: BOTHWELL, A. L. M., PASKIND, M., RETH, M., IMANISHI-KARI, T., RAJEWSKY, K. & BALTIMORE, D. (1982) NATURE, 298, 380-382. (CHECKED BY AUTHOR 01/31/83)
- 7) MOPC315: BURSTEIN, Y. & SCHECHTER, I. (1977) BIOCHEM. J., 165, 347-354; BURSTEIN, Y. & SCHECHTER, I. (1978) BIOCHEMISTRY, 17, 2392-2400. (CHECKED BY AUTHOR 08/29/79)
- 8) WES-IG13' CL: TONEGAWA, S., MAXAM, A. M., TIZARD, R., BERNARD, O. & GILBERT, W. (1978) PROC. NAT. ACAD. SCI. USA, 75, 1485-1489. (CHECKED BY AUTHOR 08/06/79)
- 9) SPR VL' CL: NAMI, F. & KINDT, T. J. (1987) IMMUNOGENET., 26, 291-295.
- 10) Y31' CL: SANCHEZ, P., MARCHE, P. N., LE GUERN, C. & CAZENAVE, P.-A. (1987) PROC. NAT. ACAD. SCI. USA, 84, 9185-9188; SANCHEZ, P., MARCHE, P. N., RUEFF-JUY, D. & CAZENAVE, P.-A. (1990) J. IMMUNOL., 144, 2816-2820.
- 11) MOPC-1' CL: ALONSO, A., HOZUMI, N. & MURIALDO, H. (1985) J. IMMUNOL., 135, 1, 614-619. (CHECKED BY AUTHOR 09/26/85)
- 12) MOPC315-26' CL: WU, G. E., GOVINDJI, N., HOZUMI, V. & MURIALDO, H. (1982) NUC. ACIDS RES., 10, 3831-3843. (CHECKED BY AUTHOR 05/30/83)

GENERAL NOTES: SIGNAL PEPTIDES OF MOUSE LAMBDA LIGHT CHAINS

THE NUCLEOTIDE SEQUENCES OF DIFFERENT CLONES CONTAIN AN INTERVENING SEQUENCE OF NONTRANSLATED BASES OF VARYING LENGTHS. THE SPLICING OUT OF THESE INTRONS COULD OCCUR BETWEEN AMINO ACID POSITIONS -5 AND -4, OR -4 AND -3 OR WITHIN POSITION -4. HOWEVER, IF THE SPLICING REQUIRES GT AT THE 5'-END AND AG AT THE 3'-END OF THE INTRON, THIS WOULD DEFINE THE JOINING AS OCCURRING WITHIN THE CODON OF AMINO ACID RESIDUE -4. THE INTRON SIZES OF DIFFERENT SEQUENCES ARE LISTED BELOW:

CLONE:	SOURCE:	INTRON SIZE:
S43' CL	MOUSE MYELOMA CDNA	
IG303LAMBDA' CL	MOUSE H2020 MYELOMA DNA	93
IG99LAMBDA' CL	MOUSE EMBRYO DNA	93
WES-IG13' CL	MOUSE EMBRYO DNA	93
MOPC315-26' CL	MOUSE MYELOMA DNA	93
243' CL	CHICKEN SPLEEN CELL CDNA	

SPECIFIC NOTES: SIGNAL PEPTIDES OF MOUSE LAMBDA LIGHT CHAINS

- 7) MOPC315: IT HAS ALSO BEEN SEQUENCED BY OTHERS (JILKA, R. L. & PESTKA, S. (1979) J. BIOL. CHEM., 254, 9270-9276.); THEY FOUND SER AT POSITION -3 INSTEAD OF ALA, AND ALA AT POSITION -2 INSTEAD OF SER. THE LISTED SEQUENCE IS IN AGREEMENT WITH THAT TRANSLATED FROM THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE MYELOMA CDNA (BOTHWELL, A. L. M., PASKIND, M., RETH, M., IMANISHI-KARI, T., RAJEWSKY, K. & BALTIMORE, D. (1982) NATURE, 298, 380-382).
- 10) Y31' CL: THIS IS A NEW MOUSE LAMBDA LIGHT CHAIN GENE DESIGNATED AS lambda x.

SIGNAL PEPTIDES OF MISCELLANEOUS

INVARIANT RESIDUES	1 YTH	2 IR	3 Y3-AG
	34	5HL	102 1.2.3 'CL
-29	---	---	---
-28	---	---	---
-27	---	---	---
-26	---	---	---
-25	---	---	---
-24	---	---	MET
-23	---	---	GLY
-22	---	---	VAL
-21	---	---	MET ARG
-20	---	---	MET MET ME
-19	---	---	ALA GLU GI
-18	---	---	ALA SER SI
-17	---	---	LEU HIS GI
-16	---	---	GLN THR TI
-15	---	---	LEU ARG G
-14	---	---	LEU VAL V
-13	---	---	GLY PHE L
-12	---	---	VAL ILE M
-11	---	---	ALA PHE S
-10	---	---	ALA LEU I
-9	---	---	SER LEU I
-8	---	---	SER LEU I
-7	---	---	GLY TRP
-6	---	---	SER LEU
-5	---	---	GLN SER
-4	---	---	ALA GLY
-3	---	---	MET THR
-2	---	---	ARG ASP
-1	---	---	CYS GLY

SIGNAL PEPTIDES OF MISCELLANEOUS KAPPA LIGHT CHAINS

	INVARIANT RESIDUES	1 YTH 34.5HL 'CL	2 IR- 102	3 Y3-Ag 1.2.3. 'CL	4 IR- 52	5 IR- 487A	6 IR- 487B	7 V18A 'CL	8 V20 'CL	9 17D9 'CL	10 V19A 'CL	11 V18B 'CL	12 3C8 'CL	13 V19B 'CL	14 RMH 12F2	15 12F2 B2'CL	16 RAB B5'CL	17 HORNED SHARK 1122 'CL	# OF SEQUENCES	# OF AMINO ACIDS
-29		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1	1
-28		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1	1
-27		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	9	2
-26		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	8	3
-25		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	12	2
-24		---	MET	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	10	4
-23		---	GLY	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	9	2
-22		---	VAL	---	---	MET	---	MET	MET	---	MET	MET	---	---	---	---	---	---	8	3
-21		MET	ARG	---	---	ASP	---	ASP	ASP	---	ASP	ASP	---	---	---	---	---	---	12	2
-20		MET	MET	MET	MET	MET	---	THR	THR	---	THR	THR	---	---	---	---	THR	---	10	4
-19		ALA	GLU	GLU	MET	---	---	ARG	ARG	---	ARG	ARG	---	---	---	---	ARG	---	10	4
-18		ALA	SER	SER	---	---	---	ALA	ALA	---	ALA	ALA	---	---	---	---	ALA	---	9	2
-17		LEU	HIS	GLN	PRO	---	---	PRO	PRO	---	PRO	PRO	---	---	---	---	PRO	---	10	4
-16		GLN	THR	THR	---	---	---	THR	THR	---	THR	THR	---	---	---	---	ALA	MET	10	4
-15		LEU	ARG	GLN	---	---	---	GLN	GLN	---	GLN	GLN	---	---	---	---	GLN	TYR	10	4
-14		LEU	VAL	VAL	LEU	---	---	LEU	LEU	---	LEU	LEU	---	---	---	---	LEU	LEU	15	2
-13		GLY	PHE	LEU	LEU	---	---	LEU	LEU	---	LEU	LEU	---	---	---	---	LEU	LEU	17	3
-12		VAL	ILE	MET	---	---	---	GLY	GLY	---	GLY	GLY	---	---	---	---	GLY	GLY	14	4
-11		ALA	PHE	SER	LEU	---	---	LEU	LEU	---	LEU	LEU	---	---	---	---	LEU	THR	15	5
-10		ALA	LEU	LEU	LEU	LEU	---	LEU	LEU	---	LEU	LEU	---	---	---	---	LEU	LEU	17	2
-9		SER	LEU	LEU	LEU	LEU	---	LEU	LEU	---	LEU	LEU	---	---	---	---	LEU	LEU	17	2
-8		SER	LEU	LEU	LEU	---	---	LEU	LEU	---	LEU	LEU	---	---	---	---	LEU	LEU	17	2
-7		GLY	TRP	TRP	---	---	---	TRP	TRP	---	TRP	TRP	---	---	---	---	TRP	HIS	12	3
-6		SER	LEU	ILE	LEU	---	---	LEU	LEU	---	LEU	LEU	---	---	---	---	LEU	LEU	15	4
-5		GLN	SER	SER	PRO	---	---	PRO	PRO	---	PRO	PRO	---	---	---	---	PRO	THR	14	4
-4		ALA	GLY	GLY	---	GLY	GLY	GLY	ASP	---	GLY	GLY	---	---	---	---	GLY	GLY	15	3
-3		MET	THR	THR	MET	---	---	ALA	ALA	---	ALA	ALA	---	---	---	---	ALA	VAL	14	4
-2		ARG	ASP	CYS	---	---	---	ILE	ARG	---	ARG	THR	---	---	---	---	ARG	LEU	13	6
-1		CYS	GLY	GLY	---	---	---	CYS	CYS	---	CYS	PHE	---	---	---	---	CYS	ALA	13	4

0-9276.); THEY FOUND
ENCE IS IN AGREEMENT
LL, A. L. M., PASKIND, M.,

PRECURSOR OF:

- 1) YTH 34.5HL/CL: RAT KAPPA LIGHT CHAIN
- 2) IR-102: RAT KAPPA LIGHT CHAIN OF IR-102
- 3) Y3-Ag 1.2.3./CL: RAT KAPPA LIGHT CHAIN
- 4) IR-52: RAT KAPPA LIGHT CHAIN OF IR-52
- 5) IR-487A: RAT KAPPA LIGHT CHAIN OF IR-487 (2 DIFFERENT PRECURSORS)
- 6) IR-487B: RAT KAPPA LIGHT CHAIN OF IR-487 (2 DIFFERENT PRECURSORS)
- 7) V18A/CL: RABBIT KAPPA LIGHT CHAIN
- 8) V20/CL: RABBIT KAPPA LIGHT CHAIN
- 9) 17D9/CL: RABBIT KAPPA LIGHT CHAIN
- 10) V19A/CL: RABBIT KAPPA LIGHT CHAIN
- 11) V18B/CL: RABBIT KAPPA LIGHT CHAIN
- 12) 3C8/CL: RABBIT KAPPA LIGHT CHAIN
- 13) V19B/CL: RABBIT KAPPA LIGHT CHAIN
- 14) RMH 12F2: RABBIT KAPPA LIGHT CHAIN
- 15) 12F2 B2/CL: RABBIT KAPPA LIGHT CHAIN
- 16) RAB B5/CL: RABBIT KAPPA LIGHT CHAIN
- 17) HORNED SHARK 1122/CL: HORNED SHARK KAPPA LIGHT CHAIN

REFERENCE: SIGNAL PEPTIDES OF MISCELLANEOUS KAPPA LIGHT CHAINS

- 1) YTH 34.5HL/CL: RIECHMANN, L., CLARK, M., WALDMANN, H. & WINTER, G. (1988) NATURE, 332, 323-327.
- 2) IR-102: BURSTEIN, Y., BAZIN, H. & SCHECHTER, I. (1979) ISRAEL J. MED. SCI., 15, 101-102; SCHECHTER, I., WOLF, O., ZEMELL, R. & BURSTEIN, Y. (1979) FED. PROC., 38, 1839-1845. (CHECKED BY AUTHOR 08/29/79)
- 3) Y3-Ag 1.2.3./CL: CROWE, J.S., SMITH, M.A. & COOPER, H.J. (1989) NUCL. ACIDS RES., 17, 7992.
- 4) IR-52: BURSTEIN, Y., BAZIN, H., ZIV, E., KANTOR, F. & SCHECHTER, I. (1982) BIOCHEM. BIOPHYS. RES. COMMUN., 105, 1408-1415. (CHECKED BY AUTHOR 12/15/82)
- 5) IR-487A: BURSTEIN, Y., BAZIN, H., ZIV, E., KANTOR, F. & SCHECHTER, I. (1982) BIOCHEM. BIOPHYS. RES. COMMUN., 105, 1408-1415. (CHECKED BY AUTHOR 12/15/82)
- 6) IR-487B: BURSTEIN, Y., BAZIN, H., ZIV, E., KANTOR, F. & SCHECHTER, I. (1982) BIOCHEM. BIOPHYS. RES. COMMUN., 105, 1408-1415. (CHECKED BY AUTHOR 12/15/82)
- 7) V18A/CL: HEIDMANN, O. & ROUGEON, F. (1984) NATURE, 311, 74-76.
- 8) V20/CL: LIEBERMAN, R., EMORINE, L. & MAX, E.E. (1984) J. IMMUN., 133, 5, 2753-2756.
- 9) 17D9/CL: MCCARTNEY-FRANCIS, N., SKURLA, R.M., JR., MAGE, R.E. & BERNSTEIN, K.E. (1984) PROC. NAT. ACAD. SCI. USA, 81, 1794-1798.
- 10) V19A/CL: HEIDMANN, O. & ROUGEON, F. (1984) NATURE, 311, 74-76.
- 11) V18B/CL: HEIDMANN, O. & ROUGEON, F. (1984) NATURE, 311, 74-76.
- 12) 3C8/CL: BERNSTEIN, K.E., LAMOYI, E., MCCARTNEY-FRANCIS, N. & MAGE, R.G. (1984) J. EXP. MED., 159, 635-640.
- 13) V19B/CL: HEIDMANN, O. & ROUGEON, F. (1984) NATURE, 311, 74-76.
- 14) RMH 12F2: DREHER, K.L., SOGN, J.A., GATES, F.T., III, KUO, M.C. & KINDT, T.J. (1983) J. IMMUNOL., 130, 442-448.
- 15) 12F2 B2/CL: HEIDMANN, O., AUFRAY, C., CAZENAVE, P.A. & ROUGEON, F. (1981) PROC. NAT. ACAD. SCI. USA, 78, 5802-5806; DREHER, K.L., EMORINE, L., KINDT, T.J. & MAX, E.E. (1983) PROC. NAT. ACAD. SCI. USA, 80, 4489-4493; DREHER, K.L., SOGN, J.A., GATES, F.T., III, KUO, M.C. & KINDT, T.J. (1983) J. IMMUNOL., 130, 442-448. (CHECKED BY AUTHOR 07/01/85)
- 16) RAB B5/CL: BERNSTEIN, K.E., SKURLA, R.M., JR. & MAGE, R.G. (1983) NUC. ACIDS RES., 11, 7205-7214.
- 17) HORNED SHARK 1122/CL: SHAMBLOTT, M.J. & LITMAN, G.W. (1989) EMBO J., 8, 3733-3739.

GENERAL NOTES: SIGNAL PEPTIDES OF MISCELLANEOUS KAPPA LIGHT CHAINS

THE NUCLEOTIDE SEQUENCES OF DIFFERENT CLONES CONTAIN AN INTERVENING SEQUENCE OF NONTRANSLATED BASES OF VARYING LENGTHS. THE SPLICING OUT OF THESE INTRONS COULD OCCUR BETWEEN AMINO ACID POSITIONS -5 AND -4, OR -4 AND -3, OR WITHIN POSITION -4. HOWEVER, IF THE SPLICING REQUIRES GT AT THE 5'-END AND AG AT THE 3'-END OF THE INTRON, THIS WOULD DEFINE THE JOINING AS OCCURRING WITHIN THE CODON OF AMINO ACID RESIDUE -4. THE INTRON SIZES OF DIFFERENT SEQUENCES ARE LISTED BELOW:

CLONE:	SOURCE:	INTRON SIZE:
HK100/CL	HUMAN FETAL LIVER DNA	118
HK101/CL	HUMAN FETAL LIVER DNA	125
HK102/CL	HUMAN FETAL LIVER DNA	125
MOFC173B/CL	MOUSE ADULT DNA	121
S107B/CL	MOUSE ADULT MYELOMA DNA	175
L8/CL	MOUSE ADULT LIVER DNA	175
K2/CL	MOUSE EMBRYO DNA	118
MPC11/CL	MOUSE ADULT DNA	242
VKAPPA167/CL	MOUSE ADULT LIVER DNA	365
L6/CL	MOUSE ADULT LIVER DNA	113
L7/CL	MOUSE ADULT LIVER DNA	206
T1/CL	MOUSE ADULT MYELOMA DNA	113
T2/CL	MOUSE ADULT MYELOMA DNA	215
VT1/B/CL	MOUSE ADULT MYELOMA DNA	113
VTNP/CL	MOUSE HYBRIDOMA DNA	177

SPECIFIC NOTES: SIGNAL PEPTIDES OF MISCELLANEOUS KAPPA LIGHT CHAINS

- 14) RMH 12F2: THIS IS OBTAINED FROM A RABBIT-MOUSE HYBRIDOMA (RMH).
- 15) 12F2 B2/CL: POSITIONS -22, -14, -13, -11 TO -8 WERE DETERMINED BY AMINO ACID SEQUENCING. THE CONSTANT REGION IS CALLED RABBIT K184/CL. THE AUTHORS ALSO CALL THIS SEQUENCE FB4D5.

SIGNAL PEPTIDES OF MISCELLANEOUS KAPPA LIGHT CHAINS

INVARIA	RESIDUES	1 RAT VL 'CL	2 PDH7 'CL	3 VL3 'CL	4 F
-21	MET	---	---	---	---
-20		MET	MET	MET	
-19		THR	ALA	ALA	
-18		CYS	CYS	CYS	
-17		THR	THR	THR	
-16		SER	PRO	PRO	
-15	LEU	LEU	LEU	LEU	
-14	LEU	LEU	LEU	LEU	
-13		LEU	LEU	LEU	
-12		ILE	LEU	LEU	
-11	LEU	---	LEU	LEU	
-10		LEU	THR	THR	
-9		LEU	LEU	LEU	
-8		ALA	LEU	LEU	
-7		VAL	GLN	GLN	
-6		CYS	CYS	SER	
-5		THR	THR	THR	
-4		GLY	GLY	GLY	
-3		ALA	SER	SER	
-2		ILE	LEU	LEU	
-1		SER	SER	SER	

22 CLONE ES 'CL	23 CLONE S 'CL	24 CLONE 12 'CL	25 CHICK V1 'CL
-21			
-20			
-19			
-18			
-17			
-16			
-15			
-14			
-13			
-12			
-11			
-10			
-9			
-8			
-7			
-6	SER	SER	SER
-5	LEU	LEU	LEU
-4	VAL	VAL	VAL
-3	GLN	GLN	GLN
-2	ALA	ALA	ALA
-1	ALA	ALA	ALA

SIGNAL PEPTIDES OF MISCELLANEOUS LAMBDA LIGHT CHAINS

INVARIANT RESIDUES	1 RAT VL 'CL	2 PDH7 CL 'CL	3 FVL3 CL 'CL	4 PDH8 CL 'CL	5 FVL2 CL 'CL	6 G4 CL 'CL	7 G4 CL 'CL	8 S11 CL 'CL	9 IOL CL 'CL	10 B19/gl CL 'CL	11 bu 36 CL 'CL	12 sp 126 CL 'CL	13 243 CL 'CL	14 H18 CL 'CL	15 H13 CL 'CL	16 H11 CL 'CL	17 bu 24 CL 'CL	18 bu 2 CL 'CL	19 sp 1 CL 'CL	20 SHEEP PSLC CL 'CL	21 CHICKEN LAMBDA 1 CL 'CL
-21	MET	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-20	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
-19	THR	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
-18	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
-17	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
-16	LEU	SER	PRO	PRO	PRO	PRO	PRO	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-15	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-14	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
-13	LEU	LEU	LEU	LEU	LEU	LEU	LEU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-12	ILE	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-11	LEU	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
-10	LEU	THR	THR	THR	THR	THR	THR	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
-9	LEU	LEU	LEU	LEU	LEU	LEU	LEU	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS
-8	ALA	LEU	LEU	LEU	LEU	LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
-7	VAL	GLN	GLN	GLN	GLN	GLN	GLN	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
-6	CYS	CYS	SER	SER	SER	SER	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
-5	SER	THR	THR	THR	THR	THR	THR	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
-4	GLY	GLY	GLY	GLY	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-3	ALA	SER	SER	SER	SER	SER	SER	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-2	ILE	LEU	LEU	LEU	LEU	LEU	LEU	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
-1	SER	SER	SER	SER	SER	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA

OLF, O., ZEMELL, R. &

105,1408-1415. (CHECKED

..105,1408-1415.

..105,1408-1415.

CI, USA, 81.1794-1798.

48.

802-5806; DREHER, K.L.,
SOGN, J.A., GATES, F.T., III.ASES OF VARYING LENGTHS.
OR WITHIN POSITION -4.
EFINE THE JOINING AS
LISTED BELOW:

	22 CLONE E5 'CL	23 CLONE 5 'CL	24 CLONE 12 'CL	25 CHICKEN V1 'CL	26 CHICKEN V2 'CL	27 CHICKEN V3 'CL	# OF SEQUENCES	# OF AMINO ACIDS
-21							3	1
-20							8	2
-19							8	3
-18							8	3
-17							8	3
-16							9	1
-15							9	1
-14							11	2
-13							11	4
-12							9	1
-11							11	3
-10							11	3
-9							11	3
-8							12	4
-7							12	3
-6							27	4
-5	SER	SER	SER	PRO	SER	ALA	27	4
-4	LEU	LEU	LEU	ARG	LEU	TYR	27	4
-3	VAL	VAL	VAL	LEU	VAL	SER	27	4
-2	GLN	GLN	GLN	TRP	GLN	ARG	27	5
-1	ALA	ALA	ALA	ASP	ALA	GLY	27	4

STANT REGION IS CALLED

PRECURSOR OF:

- 1) RAT VL/CL: RAT LAMBDA LIGHT CHAIN
- 2) pDH7/CL: BASILEA RABBIT LAMBDA LIGHT CHAIN
- 3) rVL3/CL: RABBIT LAMBDA LIGHT CHAIN
- 4) pDH8/CL: BASILEA RABBIT LAMBDA LIGHT CHAIN
- 5) rVL2/CL: RABBIT LAMBDA LIGHT CHAIN
- 6) G4/CL: CHICKEN LAMBDA LIGHT CHAIN
- 7) G4 GERMLINE/CL: CHICKEN LAMBDA LIGHT CHAIN
- 8) S11/CL: CHICKEN LAMBDA LIGHT CHAIN
- 9) Ig1/CL: CHICKEN LAMBDA LIGHT CHAIN
- 10) B19/g1/CL: CHICKEN LAMBDA LIGHT CHAIN
- 11) bu 36/CL: CHICKEN LAMBDA LIGHT CHAIN
- 12) sp 126/CL: CHICKEN LAMBDA LIGHT CHAIN
- 13) 243/CL: CHICKEN LAMBDA LIGHT CHAIN
- 14) H18/CL: CHICKEN LAMBDA LIGHT CHAIN
- 15) H13/CL: CHICKEN LAMBDA LIGHT CHAIN
- 16) H11/CL: CHICKEN LAMBDA LIGHT CHAIN
- 17) bu 24/CL: CHICKEN LAMBDA LIGHT CHAIN
- 18) bu 2/CL: CHICKEN LAMBDA LIGHT CHAIN
- 19) sp 1/CL: CHICKEN LAMBDA LIGHT CHAIN
- 20) SHEEP pSLC/CL: SHEEP LAMBDA CHAIN
- 21) CHICKEN LAMBDA 1/CL: CHICKEN LAMBDA LIGHT CHAIN
- 22) CLONE E5/CL: CHICKEN LAMBDA LIGHT CHAIN
- 23) CLONE 5/CL: CHICKEN LAMBDA LIGHT CHAIN
- 24) CLONE 12/CL: CHICKEN LAMBDA LIGHT CHAIN
- 25) CHICKEN V1/CL: CHICKEN V1 IN PSEUDOGENES OF VARIABLE REGION
- 26) CHICKEN V2/CL: CHICKEN V2 IN PSEUDOGENES OF VARIABLE REGION
- 27) CHICKEN V3/CL: CHICKEN V3 IN PSEUDOGENES OF VARIABLE REGION

REFERENCE: SIGNAL PEPTIDES OF MISCELLANEOUS LAMBDA LIGHT CHAINS

- 1) RAT VL/CL: STEEN, M.-L., HELLMAN, L. & PETTERSSON, U. (1987) GENE, 55, 75-84.
- 2) pDH7/CL: HAYZER, D.J. & JATON, J.-C. (1987) J. IMMUNOL., 138, 2316-2322. (CHECKED BY AUTHOR 07/13/87)
- 3) rVL3/CL: HAYZER, D.J. & JATON, J.-C. (1989) GENE, 80, 185-191.
- 4) pDH8/CL: HAYZER, D.J. & JATON, J.-C. (1989) GENE, 80, 185-191.
- 5) rVL2/CL: HAYZER, D.J. & JATON, J.-C. (1989) GENE, 80, 185-191.
- 6) G4/CL: KIM, S., HUMPHRIES, E.H., TJOELKER, L., CARLSON, L. & THOMPSON, C.B. (1990) MOL. CELL. BIOL., 10, 3224-3231.
- 7) G4 GERMLINE/CL: KIM, S., HUMPHRIES, E.H., TJOELKER, L., CARLSON, L. & THOMPSON, C.B. (1990) MOL. CELL. BIOL., 10, 3224-3231.
- 8) S11/CL: PARVARI, R., ZIV, E., LANTNER, F., TEL-OR, S., BURSTEIN, Y. & SCHECHTER, I. (1987) EMBO J., 6, 97-102.
- 9) Ig1/CL: MCCORMACK, W.T., TJOELKER, L.W., CARLSON, L.M., PETRYNIAK, B., BARTH, C.F., HUMPHRIES, E.H. & THOMPSON, C.B. (1989) CELL, 56, 785-791.
- 10) B19/g1/CL: PARVARI, R., ZIV, E., LANTNER, F., HELLER, D. & SCHECHTER, I. (1990) PROC. NATL. ACAD. SCI. USA, 87, 3072-3076.
- 11) bu 36/CL: PARVARI, R., ZIV, E., LANTNER, F., HELLER, D. & SCHECHTER, I. (1990) PROC. NATL. ACAD. SCI. USA, 87, 3072-3076.
- 12) sp 126/CL: PARVARI, R., ZIV, E., LANTNER, F., HELLER, D. & SCHECHTER, I. (1990) PROC. NATL. ACAD. SCI. USA, 87, 3072-3076.
- 13) 243/CL: REYNAUD, C.A., DAHAN, A. & WEILL, J.-C. (1983) PROC. NATL. ACAD. SCI. USA, 80, 4099-4103. (CHECKED BY AUTHOR 02/22/85)
- 14) H18/CL: PARVARI, R., ZIV, E., LANTNER, F., TEL-OR, S., BURSTEIN, Y. & SCHECHTER, I. (1987) EMBO J., 6, 97-102.
- 15) H13/CL: PARVARI, R., ZIV, E., LANTNER, F., TEL-OR, S., BURSTEIN, Y. & SCHECHTER, I. (1987) EMBO J., 6, 97-102.
- 16) H11/CL: PARVARI, R., ZIV, E., LANTNER, F., HELLER, D. & SCHECHTER, I. (1990) PROC. NATL. ACAD. SCI. USA, 87, 3072-3076.
- 17) bu 24/CL: PARVARI, R., ZIV, E., LANTNER, F., HELLER, D. & SCHECHTER, I. (1990) PROC. NATL. ACAD. SCI. USA, 87, 3072-3076.
- 18) bu 2/CL: PARVARI, R., ZIV, E., LANTNER, F., HELLER, D. & SCHECHTER, I. (1990) PROC. NATL. ACAD. SCI. USA, 87, 3072-3076.
- 19) sp 1/CL: PARVARI, R., ZIV, E., LANTNER, F., HELLER, D. & SCHECHTER, I. (1990) PROC. NATL. ACAD. SCI. USA, 87, 3072-3076.
- 20) SHEEP pSLC/CL: FOLEY, R.C. & BEH, K.J. (1989) J. IMMUNOL., 142, 708-711.
- 21) CHICKEN LAMBDA 1/CL: REYNAUD, C.-A., ANQUEZ, V., DAHAN, A. & WEILL, J.-C. (1985) CELL, 40, 283-291.
- 22) CLONE E5/CL: KIM, S., HUMPHRIES, E.H., TJOELKER, L., CARLSON, L. & THOMPSON, C.B. (1990) MOL. CELL. BIOL., 10, 3224-3231.
- 23) CLONE 5/CL: KIM, S., HUMPHRIES, E.H., TJOELKER, L., CARLSON, L. & THOMPSON, C.B. (1990) MOL. CELL. BIOL., 10, 3224-3231.
- 24) CLONE 12/CL: KIM, S., HUMPHRIES, E.H., TJOELKER, L., CARLSON, L. & THOMPSON, C.B. (1990) MOL. CELL. BIOL., 10, 3224-3231.
- 25) CHICKEN V1/CL: REYNAUD, C.-A., ANQUEZ, V., DAHAN, A. & WEILL, J.-C. (1985) CELL, 40, 283-291.
- 26) CHICKEN V2/CL: REYNAUD, C.-A., ANQUEZ, V., DAHAN, A. & WEILL, J.-C. (1985) CELL, 40, 283-291.
- 27) CHICKEN V3/CL: REYNAUD, C.-A., ANQUEZ, V., DAHAN, A. & WEILL, J.-C. (1985) CELL, 40, 283-291.

GENERAL NOTES: SIGNAL PEPTIDES OF MISCELLANEOUS LAMBDA LIGHT CHAINS

THE NUCLEOTIDE SEQUENCES OF DIFFERENT CLONES CONTAIN AN INTERVENING SEQUENCE OF NONTRANSLATED BASES OF VARYING LENGTHS. THE SPLICING OUT OF THESE INTRONS COULD OCCUR BETWEEN AMINO ACID POSITIONS -5 AND -4, OR -4 AND -3, OR WITHIN POSITION -4. HOWEVER, IF THE SPLICING REQUIRES GT AT THE 5'-END AND AG AT THE 3'-END OF THE INTRON, THIS WOULD DEFINE THE JOINING AS OCCURRING WITHIN THE CODON OF AMINO ACID RESIDUE -4. THE INTRON SIZES OF DIFFERENT SEQUENCES ARE LISTED BELOW:

CLONE:	SOURCE:	INTRON SIZE:
S43/CL	MOUSE MYELOMA CDNA	
IG303/LAMBDA/CL	MOUSE H2020 MYELOMA DNA	93
IG99/LAMBDA/CL	MOUSE EMBRYO DNA	93
WES-IG13/CL	MOUSE EMBRYO DNA	93
MOPC315-26/CL	MOUSE MYELOMA DNA	93
243/CL	CHICKEN SPLEEN CELL CDNA	

SPECIFIC NOTES: SIGNAL PEPTIDES OF MISCELLANEOUS LAMBDA LIGHT CHAINS

- 2) pDH7/CL: ISOLATED FROM SPLEEN OF BASILEA RABBIT HYPERIMMUNIZED WITH TYPE II PNEUMOCOCCAL POLYSACCHARIDE.
- 8) S11/CL: FROM CDNA OF CHICKEN SPLEEN.
- 14) H18/CL: FROM CDNA OF CHICKEN HARDER GLAND (A GLAND ENRICHED WITH IMMUNOCYTES).
- 15) H13/CL: FROM CDNA OF CHICKEN HARDER GLAND (A GLAND ENRICHED WITH IMMUNOCYTES).
- 16) H11/CL: FROM CDNA OF CHICKEN HARDER GLAND (A GLAND ENRICHED WITH IMMUNOCYTES).
- 20) SHEEP pSLC/CL: TRANSLATED FROM CDNA OF SHEEP LYMPHOCYTES

SIGNAL PEPTIDES OF HUMAN HEAVY

INVARIA	1	2	3	4
RESIDUES	21-2	2-1	1-92	V
	'CL	'CL	'CL	'CL
-20	MET	MET	MET	MET
-19	ASP	ASP	ASP	ASP
-18	TRP	TRP	TRP	TRP
-17	THR	THR	THR	THR
-16	TRP	TRP	TRP	TRP
-15	VAL	VAL	VAL	VAL
-14	PHE	PHE	PHE	PHE
-13	CYS	CYS	CYS	CYS
-12				
-11				
-10	LEU	LEU	LEU	LEU
-9	LEU	LEU	LEU	LEU
-8	ALA	ALA	ALA	ALA
-7	VAL	VAL	VAL	VAL
-6	ALA	ALA	ALA	ALA
-5	PRO	PRO	PRO	PRO
-4	GLY	GLY	GLY	GLY
-3	ALA	ALA	ALA	ALA
-2	HIS	HIS	HIS	HIS
-1	SER	SER	SER	SER

22	23	24	25
ND	189/F2	71-5	VH251
'CL	'CL	'CL	'CL

-20	MET	MET	MET	MET
-19	ASP	ASP	ASP	ASP
-18	TRP	TRP	TRP	TRP
-17	THR	THR	THR	THR
-16	TRP	TRP	TRP	TRP
-15	SER	ARG	ARG	ARG
-14	ILE	ILE	ILE	ILE
-13	LEU	LEU	LEU	LEU
-12	PHE	PHE	PHE	PHE
-11				
-10	LEU	LEU	LEU	LEU
-9	VAL	VAL	VAL	VAL
-8	ALA	ALA	ALA	ALA
-7	ALA	ALA	ALA	ALA
-6	ALA	ALA	ALA	ALA
-5	THR	THR	THR	THR
-4	ARG	GLY	GLY	GLY
-3	VAL	ALA	ALA	ALA
-2	HIS	HIS	HIS	CYS
-1	SER	SER	SER	ALA

43	44	45	46	4
C6B2	58P2	SUP-T1	11	7
'CL	'CL	'CL	'CL	'CL

-20	MET	MET	MET	MET
-19	LYS	LYS	LYS	LYS
-18	HIS	HIS	HIS	HIS
-17	LEU	LEU	LEU	LEU
-16	TRP	TRP	TRP	TRP
-15	PHE	PHE	PHE	PHE
-14	PHE	PHE	PHE	PHE
-13	LEU	LEU	LEU	LEU
-12	LEU	LEU	LEU	LEU
-11				
-10	LEU	LEU	LEU	LEU
-9	VAL	VAL	VAL	VAL
-8	ALA	ALA	ALA	ALA
-7	ALA	ALA	ALA	ALA
-6	PRO	PRO	PRO	PRO
-5	ARG	ARG	ARG	ARG
-4	TRP	TRP	TRP	TRP
-3	VAL	VAL	VAL	VAL
-2	LEU	LEU	LEU	LEU
-1	SER	SER	SER	SER

66	67	68	69
Ab25	RF-KL1	Ab21	Vh38
'CL	'CL	'CL	'CL

-20	MET	MET	MET	MET
-19	GLU	GLU	GLU	GLU
-18	PHE	PHE	PHE	PHE
-17	GLY	GLY	GLY	GLY
-16	LEU	LEU	LEU	LEU
-15	SER	SER	ARG	SER
-14	TRP	TRP	TRP	TRP
-13	LEU	LEU	LEU	LEU
-12	PHE	PHE	PHE	PHE
-11				
-10	LEU	LEU	LEU	LEU
-9	VAL	VAL	VAL	VAL
-8	ALA	ALA	ALA	ALA
-7	ILE	ILE	ILE	ILE
-6	LEU	LEU	LEU	LEU
-5	LYS	LYS	LYS	LYS
-4	GLY	GLY	GLY	GLY
-3	VAL	VAL	VAL	VAL
-2	GLN	GLN	GLN	GLN
-1	CYS	CYS	CYS	CYS

SIGNAL PEPTIDES OF HUMAN HEAVY CHAINS

SIGNAL PEPTIDES OF HUMAN HEAVY CHAINS																									
	INVARIANT RESIDUES	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21			
		21- 'CL	2-1 'CL	3-1 'CL	1-92 'CL	V35 'CL	H53 'CL	E3-10 'CL	W1L2 'CL	L52 'CL	L53 'CL	L51 'CL	L54 'CL	RF-TS3 'CL	51P1 'CL	hV1263 'CL	783C 'CL	EVI-15 'CL	X17115 'CL	AND 'CL	NR1 'CL	NR2 'CL	RF-TS1 'CL	H21 'CL	ASP 'CL
-20	MET																							MET	MET
-19																								ASP	ASP
-18																								TRP	TRP
-17																								TRP	TRP
-16																								TRP	TRP
-15																								ARG	ARG
-14																								PHE	PHE
-13																								PHE	PHE
-12																								CYS	CYS
-11																								LEU	LEU
-10																								VAL	VAL
-9																								ALA	ALA
-8																								ALA	ALA
-7																								VAL	VAL
-6																								ALA	ALA
-5																								PRO	PRO
-4																								GLY	GLY
-3																								ALA	ALA
-2																								HIS	HIS
-1																								SER	SER

[illegible]

'4-3231.
 FL., 10, 3224-3231.
 12.
 'SON, C.B. (1989) CELL, 56,
 17, 3072-3076.

[illegible]

USES OF VARYING LENGTHS:
OR WITHIN POSITION -4.
REFINE THE JOINING AS
LISTED BELOW:

[illegible]

CHARIDE.

SIGNAL PEPTIDES OF HUMAN HEAVY CHAINS (cont'd)

	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108
	KIM46H	FL2-2	RF-SJ2	RF-TS2	RF-SJ1	HN-14	333	1B11	112	VH10.7	K6H6	K4B8	K5B8	K5G5	K5C7	K6P5	LY47	LY91	CE-114	V201
	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL
-20				MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
-19				GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
-18		PHE		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
-17		GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
-16		LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-15		SER		SER	SER	SER	SER	THR	THR	SER	SER	SER	SER	SER	SER	ASN	SER	GLY		
-14	TRP	TRP		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
-13	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	ILE	ILE	ILE	ILE	ILE	ILE	ILE	VAL	VAL	VAL	ARG
-12	PHE	PHE		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
-11																				
-10	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-9	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-8	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
-7	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-6	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
-5	ARG	ARG		ARG	ARG	ARG	LYS	LYS	LYS	ARG	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	THR
-4	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	THR
-3	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-2	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
-1	CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	SER

OF SEQUENCES # OF AMINO ACIDS OCCURRENCES OF MOST COMMON AMINO ACID VARIABILITY

-20	94	1	94 (MET)	1.
-19	95	6	38 (GLU)	15.
-18	96	9	36 (PHE)	24.
-17	96	6	40 (GLY)	14.
-16	96	6	42 (LEU)	14.
-15	95	10	41 (SER)	23.
-14	98	6	41 (TRP)	14.
-13	99	6	55 (LEU)	11.
-12	99	3	67 (PHE)	4.4
-11	4	2	3 (PRO)	2.7
-10	99	4	86 (LEU)	4.6
-9	98	4	83 (VAL)	4.8
-8	99	5	88 (ALA)	5.6
-7	99	8	39 (ALA)	20.
-6	99	5	46 (LEU)	11.
-5	100	10	30 (LYS)	33.
-4	101	6	77 (GLY)	7.9
-3	105	3	88 (VAL)	3.6
-2	107	5	33 (GLN)	10.
-1	108	4	56 (SER)	7.7

PRECURSOR OF:

- 21-2'CL: HUMAN HEAVY CHAINS SUBG
- 3-1'CL: HUMAN HEAVY CHAINS SUBG
- 1-92'CL: HUMAN HEAVY CHAINS SUBG
- V35'CL: HUMAN HEAVY CHAINS SUBG
- BG3'CL: HUMAN HEAVY CHAINS SUBG
- E3-10'CL: HUMAN HEAVY CHAINS SUBG
- WIL2'CL: HUMAN HEAVY CHAINS SUBG
- LB2'CL: HUMAN HEAVY CHAINS SUBG
- LB5'CL: HUMAN HEAVY CHAINS SUBG
- LB1'CL: HUMAN HEAVY CHAINS SUBG
- LB4'CL: HUMAN HEAVY CHAINS SUBG
- RF-TS3'CL: HUMAN HEAVY CHAINS SUBG
- 51P1'CL: HUMAN HEAVY CHAINS SUBG
- hV1263'CL: HUMAN HEAVY CHAINS SUBG
- 783c'CL: HUMAN HEAVY CHAINS SUBG
- EVL-15'CL: HUMAN HEAVY CHAINS SUBG
- X17115'CL: HUMAN HEAVY CHAINS SUBG
- AMD'CL: HUMAN HEAVY CHAINS SUBG
- HEI'CL: HUMAN HEAVY CHAINS SUBG
- RF-TS1'CL: HUMAN HEAVY CHAINS SUBG
- BP1'CL: HUMAN HEAVY CHAINS SUBG
- ND'CL: HUMAN HEAVY CHAINS SUBG
- 1B9/F2'CL: HUMAN HEAVY CHAINS SUBG
- 71-5'CL: HUMAN HEAVY CHAINS SUBG
- VH231'CL: HUMAN HEAVY CHAINS SUBG
- 5-1R1'CL: HUMAN HEAVY CHAINS SUBG
- VHAD'CL: HUMAN HEAVY CHAINS SUBG
- WS1'CL: HUMAN HEAVY CHAINS SUBG
- VH383ex'CL: HUMAN HEAVY CHAINS SUBG
- 5-2R1'CL: HUMAN HEAVY CHAINS SUBG
- lambda IGD-1'CL: HUMAN HEAVY CHAINS SUBG
- OMM'CL: HUMAN HEAVY CHAINS SUBG
- 6-1G1'CL: HUMAN HEAVY CHAINS SUBG
- 15P1'CL: HUMAN HEAVY CHAINS SUBG
- FK-001'CL: HUMAN HEAVY CHAINS SUBG
- VHVT'CL: HUMAN HEAVY CHAINS SUBG
- VH6'CL: HUMAN HEAVY CHAINS SUBG
- Ab26'CL: HUMAN HEAVY CHAINS SUBG
- 1-9II'CL: HUMAN HEAVY CHAINS SUBG
- 12G-1'CL: HUMAN HEAVY CHAINS SUBG
- 71-2'CL: HUMAN HEAVY CHAINS SUBG
- 71-4'CL: HUMAN HEAVY CHAINS SUBG
- C6B2'CL: HUMAN HEAVY CHAINS SUBG
- 5B2'CL: HUMAN HEAVY CHAINS SUBG
- SUP-T1 V8-1A'CL: HUMAN HEAVY CHAINS SUBG
- 11'CL: HUMAN HEAVY CHAINS SUBG
- 79'CL: HUMAN HEAVY CHAINS SUBG
- Pag-1'CL: HUMAN HEAVY CHAINS SUBG
- HuVNP'CL: HUMAN HEAVY CHAINS SUBG
- HuVLYS'CL: HUMAN HEAVY CHAINS SUBG
- HuVHCAMP'CL: HUMAN HEAVY CHAINS SUBG
- RIG1'CL: HUMAN HEAVY CHAINS SUBG
- TS2'CL: HUMAN HEAVY CHAINS SUBG
- 2-1'CL: HUMAN HEAVY CHAINS SUBG
- 38'CL: HUMAN HEAVY CHAINS SUBG
- Fog-B'CL: HUMAN HEAVY CHAINS SUBG
- 6B-3C4'CL: HUMAN HEAVY CHAINS SUBG
- Ly66'CL: HUMAN HEAVY CHAINS SUBG
- DR12910-2F8'CL: HUMAN HEAVY CHAINS SUBG
- CE-1'CL: HUMAN HEAVY CHAINS SUBG
- JB12'CL: HUMAN HEAVY CHAINS SUBG
- LAMBDA-VH26'CL: HUMAN HEAVY CHAINS SUBG
- 4G12'CL: HUMAN HEAVY CHAINS SUBG
- 30P1'CL: HUMAN HEAVY CHAINS SUBG
- VH26c'CL: HUMAN HEAVY CHAINS SUBG
- Ab25'CL: HUMAN HEAVY CHAINS SUBG
- RF-XL1'CL: HUMAN HEAVY CHAINS SUBG
- Ab21'CL: HUMAN HEAVY CHAINS SUBG
- VH38CL.10'CL: HUMAN HEAVY CHAINS SUBG
- H11'CL: HUMAN HEAVY CHAINS SUBG
- 12-2'CL: HUMAN HEAVY CHAINS SUBG
- 13-2'CL: HUMAN HEAVY CHAINS SUBG
- 38P1'CL: HUMAN HEAVY CHAINS SUBG
- Ab18'CL: HUMAN HEAVY CHAINS SUBG
- GF4/1.1'CL: HUMAN HEAVY CHAINS SUBG
- 8-1B'CL: HUMAN HEAVY CHAINS SUBG
- V65-4'CL: HUMAN HEAVY CHAINS SUBG
- 9-1'CL: HUMAN HEAVY CHAINS SUBG
- 4B4'CL: HUMAN HEAVY CHAINS SUBG
- 3D6'CL: HUMAN HEAVY CHAINS SUBG
- 1-91'CL: HUMAN HEAVY CHAINS SUBG
- 60P2'CL: HUMAN HEAVY CHAINS SUBG
- 63P1'CL: HUMAN HEAVY CHAINS SUBG
- V65-2'CL: HUMAN HEAVY CHAINS SUBG
- 22-2B'CL: HUMAN HEAVY CHAINS SUBG
- 56P1'CL: HUMAN HEAVY CHAINS SUBG
- 1-9III'CL: HUMAN HEAVY CHAINS SUBG
- 2P1'CL: HUMAN HEAVY CHAINS SUBG
- KIM46H'CL: HUMAN HEAVY CHAINS SUBG
- FL2-2'CL: HUMAN HEAVY CHAINS SUBG
- RF-SJ2'CL: HUMAN HEAVY CHAINS SUBG
- RF-TS2'CL: HUMAN HEAVY CHAINS SUBG
- RF-SJ1'CL: HUMAN HEAVY CHAINS SUBG
- HN-14'CL: HUMAN HEAVY CHAINS SUBG
- 333'CL: HUMAN HEAVY CHAINS SUBG
- 1B11'CL: HUMAN HEAVY CHAINS SUBG
- K6H6'CL: HUMAN HEAVY CHAINS SUBG
- K4B8'CL: HUMAN HEAVY CHAINS SUBG
- K5B8'CL: HUMAN HEAVY CHAINS SUBG
- K5G5'CL: HUMAN HEAVY CHAINS SUBG
- K5C7'CL: HUMAN HEAVY CHAINS SUBG

PRECURSOR OF:

106 107 108
 1091 CE- V201
 'CL 114 'CL
 'CL

MET MET
 ASP ASP
 PHE CYS
 GLY THR
 LEU TRP

SER GLY
 TRP ILE ILE
 VAL LEU ARG
 PHE PHE PHE
 --- ---

LEU LEU LEU
 VAL VAL VAL
 GLY ALA ALA
 ILE ALA ALA
 LEU ALA ALA

LYS THR THR
 GLY ASP GLY
 MET VAL VAL
 GLN HIS HIS
 CYS SER SER

- 1) 21-2'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 2) 3-1'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 3) 1-92'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 4) V35'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 5) EG3'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 6) E3-10'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 7) WIL2'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 8) L82'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 9) L85'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 10) L81'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 11) L84'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 12) RF-T83'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 13) 51P1'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 14) h1263'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 15) 783a'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 16) EV1-15'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 17) K17115'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 18) AMD'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 19) BEI'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 20) RF-TS1'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 21) HP1'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 22) ND'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 23) 189/72'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 24) 71-5'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 25) V8251'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 26) 5-1R1'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 27) V8AU'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 28) W81'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 29) Vh383ex'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 30) 5-2R1'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 31) lambda IGD-1'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 32) OM4'CL: HUMAN HEAVY CHAINS SUBGROUP I
- 33) 6-1G1'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 34) 13P1'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 35) FK-001'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 36) V8V1'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 37) V86'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 38) Ab26'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 39) 1-91Y'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 40) 12G-1'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 41) 71-2'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 42) 71-4'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 43) C682'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 44) 58P2'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 45) SUP-T1 VE-JA'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 46) 11'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 47) 79'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 48) Paq-1'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 49) HuVNP'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 50) HuVHLYS'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 51) HuVHCAMP'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 52) HIG1'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 53) TS2'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 54) 2-1'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 55) 58'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 56) Fog-B'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 57) 6R-3C4'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 58) Ly66'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 59) DR12910-278'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 60) CE-1'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 61) JBL2'CL: HUMAN HEAVY CHAINS SUBGROUP II
- 62) LAMBDA-V826'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 63) 4G12'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 64) 30P1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 65) Vh26c'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 66) Ab25'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 67) RF-KL1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 68) Ab21'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 69) Vh38C1.10'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 70) H11'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 71) 12-2'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 72) 13-2'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 73) 38P1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 74) Ab18'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 75) GF4/1.1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 76) 8-1B'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 77) v65-4'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 78) 9-1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 79) 4B4'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 80) 3D6'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 81) 1-91'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 82) 60P2'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 83) 63P1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 84) v65-2'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 85) 22-2B'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 86) 56P1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 87) 1-911'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 88) 2P1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 89) KIM46B'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 90) FL2-2'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 91) RF-6J2'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 92) RF-T82'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 93) RF-6J1'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 94) BN.14'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 95) 333'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 96) 1B11'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 97) 112'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 98) V810.7'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 99) K586'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 100) K488'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 101) K588'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 102) K5G5'CL: HUMAN HEAVY CHAINS SUBGROUP III
- 103) K5C7'CL: HUMAN HEAVY CHAINS SUBGROUP III

PRECURSOR OF: (cont'd)

- 104) K6F5'CL: HUMAN HEAVY CHAINS SUBGROUP III
 105) Ly47'CL: HUMAN HEAVY CHAINS SUBGROUP III
 106) Ly91'CL: HUMAN HEAVY CHAINS SUBGROUP III

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- 85) 22-2B'CL: BERMAN, J.E. & F.W. (1988)
- 86) 56P1'CL: SCHROEDER, H.
- 87) 1-911'CL: BERMAN, J.E. & F.W. (1988)
- 88) 2P1'CL: SCHROEDER, H.
- 89) K1M46'CL: CAIRNS, E.
- 90) V12-2'CL: NICKERSON
- 91) RF-8J2'CL: PASCUAL
- 92) RF-T82'CL: PASCUAL
- 93) RF-8J1'CL: PASCUAL
- 94) H1.14'CL: DESAI, R.
- 95) 333'CL: CLEARY, M.L. (10/31/86)
- 96) 1B11'CL: CLEARY, M.L. (10/31/86)
- 97) 112'CL: CLEARY, M.L. (10/31/86)
- 98) V10.7'CL: WHITE, M.
- 99) K6H6'CL: KON, S., LE
- 100) K4B8'CL: KON, S., LE
- 101) K5B8'CL: KON, S., LE
- 102) K5G5'CL: KON, S., LE
- 103) K5C7'CL: KON, S., LE
- 104) K6F5'CL: KON, S., LE
- 105) Ly47'CL: COGNE, M.
- 106) Ly91'CL: COGNE, M.
- 107) CE-114'CL: TAKAHASHI
- 108) V201'CL: TAKAHASHI

GENERAL NOTES: SIG

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SH441'CL

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B1-8'CL

S43'CL

186-2'CL

186-1'CL

23'CL

3'CL

102'CL

145'CL

6'CL

93G7CRI4'CL

PCH105'CL

PCH108A'CL

PCH108B'CL

PCH104'CL

PCH111'CL

MOPC21H'CL

MCPC603H'CL

V11'CL

V13'CL

PMU3'CL

CAIMAN'CL

VH101'CL

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GENERAL NOTES: SIGNAL PEPTIDES OF HUMAN HEAVY CHAINS

§ THE NUCLEOTIDE SEQUENCES OF DIFFERENT CLONES CONTAIN AN INTERVENING SEQUENCE OF NONTRANSLATED BASES OF VARYING LENGTHS. THE SPLICING OUT OF THESE INTRONS COULD OCCUR BETWEEN AMINO ACID POSITIONS -5 AND -4, OR -4 AND -3, OR WITHIN POSITION -4. HOWEVER, IF THE SPLICING REQUIRES GT AT THE 5'-END AND AG AT THE 3'-END OF THE INTRON, THIS WOULD DEFINE THE JOINING AS OCCURRING WITHIN THE CODON OF AMINO ACID RESIDUE -4. THE INTRON SIZES OF DIFFERENT SEQUENCES ARE LISTED BELOW:

CLONE:	SOURCE:	INTRON SIZE:
LAMBDA-CH26'CL	HUMAN FETAL LIVER DNA	104
HG3'CL	HUMAN FETAL LIVER DNA	84
OMM'CL	HUMAN ADULT CELL LINE CDNA	
H11'CL	HUMAN PLACENTA DNA	102
H16BR'CL	HUMAN PLACENTA DNA	102
ND'CL	HUMAN MYELOMA 266BL CDNA	
MOPC141H'CL	MOUSE ADULT DNA	81
MC101'CL	MOUSE MYELOMA DNA	84
S107'CL	MOUSE ADULT CDNA	
VH441'CL	MOUSE EMBRYO DNA	101
BCL1'CL	MOUSE ADULT DNA	82
B1-8'CL	MOUSE ADULT HYBRIDOMA CDNA	
S43'CL	MOUSE ADULT HYBRIDOMA CDNA	
186-2'CL	MOUSE ADULT LIVER DNA	82
186-1'CL	MOUSE ADULT LIVER DNA	82
23'CL	MOUSE ADULT LIVER DNA	82
3'CL	MOUSE ADULT LIVER DNA	82
102'CL	MOUSE ADULT LIVER DNA	82
145'CL	MOUSE ADULT DNA	82
6'CL	MOUSE ADULT DNA	100
93G7CRI+CL	MOUSE HYBRIDOMA CDNA	
PCH105'CL	MOUSE EMBRYO DNA	82
PCH108A'CL	MOUSE EMBRYO DNA	83
PCH108B'CL	MOUSE EMBRYO DNA	83
PCH104'CL	MOUSE EMBRYO DNA	84
PCH111'CL	MOUSE EMBRYO DNA	83
MOPC21H'CL	MOUSE ADULT PLASMACYTOMA CDNA	
MCPC603H'CL	MOUSE ADULT DNA	
V1'CL	MOUSE SPERM DNA	
V11'CL	MOUSE SPERM DNA	
V13'CL	MOUSE SPERM DNA	
PHU3'CL	RABBIT ADULT SPLENIC CDNA	
CAIMAN'CL	CAIMAN ADULT GENOMIC DNA90	
VH101'CL	MOUSE ADULT DNA	84

SPECIFIC NOTES: SIGNAL PEPTIDES OF HUMAN HEAVY CHAINS

- 13) 51P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 15) 783c'CL: ALSO KNOWN AS 783'CL.
 23) 1B9'F2'CL: FROM A PATIENT WITH B CELL ACUTE LYMPHOCYTIC LEUKEMIA WITH CHARACTERISTIC t(8;14) CYTOGENETIC TRANSLOCATION AT DIAGNOSIS.
 24) 71-5'CL: THIS IS CLASSIFIED AS A PSEUDOGENE, SINCE THE INTRON IN THE PRECURSOR REGION CANNOT BE SPLICED OUT.
 31) lambda IGD-1'CL: CLASS SWITCH FROM IGM TO IGD IS PROBABLY DUE TO HOMOLOGOUS RECOMBINATION BETWEEN sigma/mu AND SIGMA/MU.
 32) OMH'CL: IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
 34) 15P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 35) FK-001'CL: IT CAN BE EXPRESSED FUNCTIONALLY IN MOUSE MYELOMA CELLS.
 44) 58P2'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 45) SUP-F1 VH-JA'CL: IT IS FROM A PATIENT SUFFERING FROM CHILDHOOD T-CELL LYMPHOMA WITH inv(14)(q11.2;q32.2). THE INVERSION ON CHROMOSOME 14 BRINGS THE VH GENE AND JA MINIGENE TOGETHER, GIVING RISE TO A HYBRID MOLECULE CONTAINING PART OF THE IMMUNOGLOBULIN GENE AND PART OF THE T-LYMPHOCYTE RECEPTOR FOR ANTIGEN GENE.
 48) Pag-1'CL: THREE-DIMENSIONAL MODEL HAS BEEN CONSTRUCTED FOR THIS ANTIBODY.
 49) HuVNP'CL: THIS IS A HYBRID HEAVY CHAIN CONSISTING OF FR'S FROM NEWB AND CDR'S FROM B1-8'CL, AN ANTI-4-HYDROXY-3-NITROPHENACETYL CAPROIC ACID MOUSE ANTIBODY. B1-8'CL HEAVY CHAIN HAS A BINDING CONSTANT OF 1.2×10^6 , AND THIS HYBRID HEAVY CHAIN HAS A BINDING CONSTANT OF 1.9×10^6 .
 56) Fog-B'CL: THREE-DIMENSIONAL MODEL HAS BEEN CONSTRUCTED FOR THIS ANTIBODY.
 57) 6H-3C4'CL: 6H-3C4 IS AN ESTABLISHED HUMAN-MOUSE HETEROHYBRIDOMA WHICH SECRETES A HUMAN IGM-LAMBDA ANTIBODY. THIS SEQUENCE IS OBTAINED BY LIGATING THE VH GENE WITH HUMAN IGG1 REGION. THE NEW HUMAN IGG1-LAMBDA ANTIBODY FULLY RETAINS THE ORIGINAL SPECIFICITY.
 60) CE-1'CL: CELL LINE CESS
 61) JBL2'CL: FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION
 63) 4G12'CL: IT RECOGNIZES A TUMOR-ASSOCIATED AND DIFFERENTIATION ANTIGEN OF MW 195,000.
 64) 30P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 73) 38P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 82) 60P2'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 83) 63P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 86) 56P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 88) 2P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
 89) KIM46H'CL: KIM4.6 CELL LINE WAS PRODUCED BY FUSION OF TONSILLAR LYMPHOID CELLS FROM A NORMAL CHILD WITH GM4672, AN IGG-KAPPA PRODUCER.
 90) FL2-2'CL: DERIVED FROM HUMAN GENOMIC DNA OF EPSTEIN-BARR VIRUS-TRANSFORMED FETAL B CELL LINE.
 95) 333'CL: FROM A HUMAN B CELL LYMPHOMA AFTER ANTI-IDIOTYPIC ANTIBODY TREATMENT.
 96) 1B11'CL: FROM A HUMAN B CELL LYMPHOMA AFTER ANTI-IDIOTYPIC ANTIBODY TREATMENT.
 97) 112'CL: FROM A HUMAN B CELL LYMPHOMA AFTER ANTI-IDIOTYPIC ANTIBODY TREATMENT.
 98) VH10.7'CL: FROM PATIENT WITH IGD-SECRETING MYELOMA. THE V- AND C-REGIONS ARE BROUGHT TOGETHER BY A HOMOLOGOUS RECOMBINATION BETWEEN 442/443-BASE-PAIR REPEATS DELETING THE C-MU.
 99) K6H6'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
 100) K4B8'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
 101) K5B8'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
 102) K5G5'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
 103) K5C7'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
 104) K6F5'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
 105) Ly47'CL: FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION
 106) Ly91'CL: FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION

SIGNAL PEPTIDES OF MOUSE HEAVY

INVARIA NT 1 2 3
 RESIDUES TP5- E7'CL H37-
 139 'CL 68'C
 #

-20	MET (1.99)	MET	MET	MET
-19		MET	MET	MET
-18		VAL	VAL	VAL
-17		LEU	LEU	LEU
-16		SER	SER	SER
-15		---	---	---
-14		LEU	LEU	LEU
-13		LEU	LEU	LEU
-12		TYR	TYR	TYR
-11		---	---	---
-10		LEU	LEU	LEU
-9		LEU	LEU	LEU
-8		THR	THR	THR
-7		ALA	ALA	ALA
-6		LEU	LEU	LEU
-5		PRO	PRO	PRO
-4		GLY	GLY	GLY
-3		ILE	ILE	PHE
-2		LEU	LEU	LEU
-1		SER	SER	SEI

21 22 23 24 25
 Lym-1 2B2 12G10 10G10 2C
 'CL 'CL 'CL 'CL 'C

-20	MET	MET	MET	MET
-19	ALA	ALA	ALA	ALA
-18	VAL	VAL	VAL	VAL
-17	LEU	LEU	LEU	LEU
-16	GLY	VAL	VAL	VAL
-15	LEU	LEU	LEU	LEU
-14	LEU	PHE	PHE	PHE
-13	LEU	LEU	LEU	LEU
-12	CYS	CYS	CYS	CYS
-11	---	---	---	---
-10	LEU	LEU	LEU	LEU
-9	VAL	VAL	VAL	VAL
-8	THR	ALA	ALA	ALA
-7	PHE	PHE	PHE	PHE
-6	PRO	PRO	PRO	PRO
-5	SER	SER	SER	SER
-4	CYS	CYS	CYS	CYS
-3	VAL	VAL	VAL	VAL
-2	LEU	LEU	LEU	LEU
-1	SER	SER	SER	SER

43 44 45 46 47
 Id 31' 1.29 1.15 3-1
 BS.7 'CL 'CL 'CL 'CL 'CL

-20	MET	MET	MET	MET	MET
-19	ASP	GLY	GLY	GLY	GLY
-18	ARG	ARG	TRP	TRP	TRP
-17	LEU	LEU	SER	SER	SER
-16	THR	THR	TRP	TRP	TRP
-15	SER	PHE	ILE	ILE	ILE
-14	SER	SER	PHE	PHE	PHE
-13	PHE	PHE	LEU	LEU	LEU
-12	LEU	LEU	PHE	PHE	PHE
-11	---	---	---	---	---
-10	LEU	LEU	LEU	LEU	LEU
-9	LEU	LEU	LEU	LEU	LEU
-8	ILE	PRO	SER	SER	SER
-7	VAL	VAL	GLY	GLY	GLY
-6	PRO	PRO	THR	THR	THR
-5	ALA	ALA	ALA	ALA	ALA
-4	TYR	TYR	GLY	GLY	GLY
-3	VAL	VAL	VAL	VAL	VAL
-2	LEU	LEU	LEU	LEU	LEU
-1	SER	SER	SER	SER	SER

66 67 68 69 70
 B13 13 30 E4 5.4.1
 H4C8 'CL 'CL 'CL 'CL 'CL

-20	MET	MET	MET	MET	MET
-19	GLU	GLY	GLY	ASP	GLY
-18	TRP	TRP	TRP	CYS	TRP
-17	PRO	SER	SER	GLY	SER
-16	LEU	ARG	ARG	ILE	CYS
-15	ILE	ILE	ILE	SER	ILE
-14	SER	PHE	PHE	LEU	ILE
-13	LEU	LEU	VAL	LEU	VAL
-12	PHE	PHE	PHE	PHE	PHE
-11	---	---	---	---	---
-10	LEU	LEU	LEU	LEU	LEU
-9	LEU	LEU	LEU	VAL	ALA
-8	SER	SER	SER	LEU	ALA
-7	GLY	ILE	ILE	ILE	ALA
-6	THR	ILE	ILE	LEU	ALA
-5	ALA	ALA	ALA	LYS	THR
-4	GLY	GLY	GLY	SER	GLY
-3	VAL	VAL	VAL	VAL	VAL
-2	GLN	HIS	HIS	HIS	HIS
-1	SER	CYS	CYS	SER	SER

SIGNAL PEPTIDES OF MOUSE HEAVY CHAINS

YTOGENETIC TRANSLOCATION

E SPLICED OUT.
EEN sigma/mu and 'SIGMA/mu.

1.2;q32.2). THE
A HYBRID MOLECULE
NTIGEN GENE.

A BINDING CONSTANT OF

BDA ANTIBODY. THIS
G1-LAMBDA ANTIBODY FULLY

OF VARIABLE REGION

HILD WITH GM4672, AN

BY A HOMOLOGOUS

OF VARIABLE REGION
OF VARIABLE REGION

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